

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:55:43 ; Search time 187 Seconds
(without alignments)
472.273 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWLLILLIIVHPGSCALW.....APLPFGSSAHLPLPPVPG 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067	100.0	201	2 AAY06403	Aay06403 Human B-c
2	1067	100.0	201	9 ADY16489	Ady16489 PRO polyp
3	1067	100.0	201	9 AEA40207	Aea40207 Human nat
4	876	82.1	190	4 AAE02769	Aae02769 Human NKp
5	876	82.1	190	8 ADO19810	Ado19810 Human PRO
6	876	82.1	190	8 ADQ30923	Adq30923 Human NKp
7	874	81.9	190	2 AAY06401	Aay06401 Human B-c
8	859	80.5	177	2 AAY06402	Aay06402 Human B-c
9	859	80.5	177	9 ADY16598	Ady16598 PRO polyp
10	713	66.8	135	5 AAE13109	Aae13109 Human NKp
11	713	66.8	369	5 AAE19110	Aae19110 Human NKp
12	632	59.2	120	4 AAE02771	Aae02771 Human NKp
13	632	59.2	120	8 ADQ30924	Adq30924 Human NKp
14	608.5	57.0	382	8 ADP48750	Adp48750 Human NKp
15	608.5	57.0	382	9 AEA40208	Aea40208 Human CD5
16	143	13.4	28	9 AEA40197	Aea40197 Peptide (
17	125.5	11.8	246	5 AAE20273	Aae20273 Human lun
18	125	11.7	212	2 AAR60134	Aar60134 CTLA4 rec
19	125	11.7	212	2 AAR77642	Aar77642 Full leng
20	125	11.7	212	2 AAY43479	Aay43479 Amino aci
21	125	11.7	212	2 AAW81584	Aaw81584 Human CTL
22	125	11.7	212	5 ABB78106	Abb78106 Amino aci
23	125	11.7	212	5 AAU75124	Aau75124 Human CTL
24	125	11.7	212	5 AAU75132	Aau75132 Human CTL

25	125	11.7	212	6 ABP56715	Abp56715 Human CTL
26	125	11.7	212	7 ADD89013	Add89013 CTLA4 rec
27	125	11.7	212	8 ADQ89550	Adq89550 CTLA4 rec
28	125	11.7	212	9 ADP95980	Adp95980 Human CTL
29	125	11.7	212	8 ADP98655	Adp98655 Human CTL
30	125	11.7	212	9 ADX08914	Adx08914 Protein s
31	123	11.5	212	5 AAU75126	Aau75126 Human CTL
32	122.5	11.5	211	2 AAW87560	Aaw87560 Human CTL
33	122	11.4	212	5 AAU75127	Aau75127 Human CTL
34	122	11.4	212	5 AAU75131	Aau75131 Human CTL
35	122	11.4	212	5 AAU75130	Aau75130 Human CTL
36	121.5	11.4	232	6 ABU08020	Abu08020 Monoclonal
37	121.5	11.4	232	7 ADF65784	Adf65784 Human ant
38	121.5	11.4	232	8 ADJ92520	Adj92520 Human SOJ
39	121	11.3	212	5 AAU75133	Aau75133 Human CTL
40	118.5	11.1	139	5 AAU75565	Aau75565 Murine T
41	118.5	11.1	223	3 AAY15129	Aay15129 Human CTL
42	118.5	11.1	223	5 AAU74509	Aau74509 Human cyt
43	118.5	11.1	223	5 AAU74508	Aau74508 Human cyt
44	118.5	11.1	223	8 ADP12469	Adp12469 Protein e
45	118.5	11.1	223	8 ADP55366	Adp55366 Human PRO

ALIGNMENTS

RESULT 1
AAY06403
ID AAY06403 standard; protein; 201 AA.
XX
AC AAY06403;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX
KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
KW signal transduction; immunomodulator; antiinflammatory;
KW autoimmune disease; inflammation; gene therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..12
FT Protein /note= "leader peptide"
FT /note= "mature protein"
FT Modified-site 42
FT /note= "N-glycosylated"
FT Modified-site 68
FT /note= "N-glycosylated"
FT Modified-site 121
FT /note= "N-glycosylated"
FT Domain 139..162
FT /note= "transmembrane domain"
FT Peptide 166..201
FT /note= "alternatively spliced C-terminal end"
XX
WO9923867-A2.
XX
XX
XX 20-MAY-1999.
XX
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59349.
XX

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PT Novel B-cell myelin oligodendrocyte glycoproteins.

PS Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells, are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 201 AA;

Query Match 100.0%; Score 1067; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWRDEV 60
Db 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWRDEV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCREVVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCREVVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRRLQPAVV 180
Db 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRRLQPAVV 180
Qy 181 PAPLPPPCGSSAHLPPVPGG 201
Db 181 PAPLPPPCGSSAHLPPVPGG 201

RESULT 2
ADY16489
ID ADY16489 standard; protein; 201 AA.

XX AC ADY16489;

XX DT 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 2295.

XX KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX KW Antiallergic; ds; gene; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH) GENENTECH INC.

XX PT Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX Claim 8; SEQ ID NO 2295; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.

XX Sequence 201 AA;

Query Match 100.0%; Score 1067; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWRDEV 60
Db 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWRDEV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCREVVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCREVVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRRLQPAVV 180
Db 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRRLQPAVV 180
Qy 181 PAPLPPPCGSSAHLPPVPGG 201
Db 181 PAPLPPPCGSSAHLPPVPGG 201

RESULT 3
AEA40207
ID AEA40207 standard; protein; 201 AA.

XX AC AEA40207;

XX DT 11-AUG-2005 (first entry)

XX DE Human natural cytotoxicity receptor, NKp30.

XX KW natural cytotoxicity receptor; natural killer cell; lymphocyte; membrane;
XX KW tumor; cell disintegration; antibody; NKp30; hyperproliferation;
XX KW cytostatic; receptor.

XX OS Homo sapiens.

XX PN WO2005051973-A2.

XX PD 09-JUN-2005.

XX PF 24-NOV-2004; 2004WO-IL001081.

XX PR 25-NOV-2003; 2003US-0524648P.

XX PA (YISS) YISSUM RES & DEV CO.

XX PT (UYNE) UNIV BEN-GURION NEGEV RES & DEV.

XX PI Mandelboim O, Porgador A;

XX DR WPI; 2005-405348/41.

XX New peptides derived from specific natural cytotoxicity receptors and
PT capable of binding to membrane-associated biomolecules of tumor cells,
PT useful for targeting tumor cells to diagnose or treat benign and/or
PT malignant tumors.

PS Disclosure; SEQ ID NO 13; 86pp; English.

XX The invention relates to isolated peptide fragments of a natural
CC cytotoxicity receptor (NCR) of natural killer (NK) cells, or active
CC fragments, analogs or derivatives, wherein the peptide fragment is
CC capable of binding to a membrane-associated biomolecule of a tumor cell,
CC and the biomolecule comprises at least one sulfated polysaccharide, and
CC serves as the binding site of the NCR mediating the lysis of tumor cells
CC by NK cells, with the proviso that the peptide is other than a full
CC length NCR polypeptide or an isolated NCR extracellular domain. Also
CC described are: (1) an antibody that recognizes an epitope on a target
CC membrane-associated biomolecule of a tumor cell, the biomolecule
CC comprising at least one sulfated polysaccharide and mediating the lysis
CC of tumor cells by NK cells via the NCR; (2) a method of targeting a tumor
CC cell in a subject via an NCR-dependent mechanism; and (3) a method of
CC identifying peptides derived from NCR which are capable of binding to a
CC membrane-associated sulfated polysaccharide of a tumor cell. The peptide
CC fragment comprises 7-120, 8-100 or less than about 50 contiguous amino
CC acids. The peptide is a fragment of NCR selected from Nkp44, Nkp30 and
CC Nkp46. It is a fragment of the D2 domain of Nkp46 comprising a sequence
CC fully defined in the specification (SEQ ID NOS: 1 and 2), or a fragment
CC of Nkp30 selected from a sequence fully defined in the specification (SEQ
CC ID NOS: 3 and 4). Alternatively, the peptide is a fragment of Nkp44
CC having a sequence fully defined in the specification (SEQ ID NO: 5). The
CC membrane-associated biomolecule is selected from a glycosaminoglycan and
CC a proteoglycan. The antibody is capable of blocking the binding of NK
CC cells via NCR to membrane-associated sulfated polysaccharide biomolecules
CC in a cell, therefore, inhibiting NCR-dependent cell lysis associated with
CC autoimmunity. The peptides and antibodies of the invention are useful for
CC targeting a tumor cell in a subject via an NCR-dependent mechanism. The
CC composition and methods of the invention are useful for targeting tumor
CC cells to diagnose and/or treat benign and malignant tumors or
CC proliferative diseases. This sequence represents human natural
CC cytotoxicity receptor, Nkp30.

XX
SQ Sequence 201 AA;

Query Match 100.0%; Score 1067; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWMLLLILMVHPGSCALWVSQPPETRTLEGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
Db 1 MAWMLLLILMVHPGSCALWVSQPPETRTLEGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60

Qy 61 VPGKEVRNGTPEFRGRPLASSRFLDHDHQLHDIRVGRGHDSIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGRPLASSRFLDHDHQLHDIRVGRGHDSIYVCRVEVLGLGVGTG 120

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSVTVYQKCLTWKGRQLPAVV 180
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSVTVYQKCLTWKGRQLPAVV 180

Qy 181 PAPLPFPCGSSAHLPPVPGG 201
Db 181 PAPLPFPCGSSAHLPPVPGG 201

RESULT 4
AAE02769
ID AAE02769 standard; protein; 190 AA.
XX
AC AAE02769;
XX
XX 06-AUG-2001 (first entry)
XX
XX Human Nkp30 receptor.
XX
XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
KW therapy.

XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18 /label= Signal_peptide
FT Protein 19..190 /label= Mature_Nkp30_receptor_protein
FT Region 19..138 /label= Extracellular_region
FT /note= "Forms an immunoglobulin (Ig) V-like domain"
FT Modified-site 42 /note= "N-glycosylation site"
FT Modified-site 121 /note= "N-glycosylation site"
FT Region 139..157 /label= Transmembrane_region
FT Region 158..190 /label= Intracellular_region
XX WO200136630-A2.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-EP011697.
XX
XX 15-NOV-1999; 99CA-02288307.
XX 15-NOV-1999; 99US-00440514.
XX
XX (INNA-) INNATE PHARMA SAS.
XX (UYGE-) UNIV GENOVA.
XX
XX Moretta A, Bottino C, Biassoni R;
XX
XX WPI; 2001-329221/34.
XX N-PSDB; AAD06564.
XX
XX Novel compound, useful for detection and/or quantifying the presence of
XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.
XX
XX Claim 1; Fig 7B; 83pp; English.
XX
XX The invention relates to human Nkp30 receptor and its corresponding cDNA
XX molecule which is involved in natural cytotoxicity mediated by natural
XX killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX useful for detecting and/or quantifying the presence of NK cells in a
XX biological sample. The invention also provide kits for detecting and/or
XX quantifying the presence of NK cells, for the selective removal of NK
XX cells from a biological sample, for the positive and selective
XX purification of NK cells from a biological sample and for the in vitro
XX stimulation of NK cell cytotoxicity. The invention further provides a
XX pharmaceutical composition which is used as a drug for grafting
XX enhancement, graft versus host (GvH) inhibition, stimulation of graft
XX versus tumour (GvT) and especially graft versus leukaemia (GvL), and for
XX the prevention, palliation and/or therapy of solid or liquid tumours,
XX such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
XX microorganism, notably viral infection. Nkp30 antibodies are useful for
XX identifying Nkp30 natural ligands and allow assessment of the level of
XX surface Nkp30 ligand expressed on an NK-susceptible target cell and the
XX comparison of this level to the standard physiological one. Hence Nkp30
XX antibodies are useful in the diagnosis of tumours or of infection. The
XX present sequence is human Nkp30 receptor

XX
SQ Sequence 190 AA;

Query Match 82.1%; Score 876; DB 4; Length 190;
Best Local Similarity 89.2%; Pred. No. 5.9e-75;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

Qy 1 MAWMLLLILMVHPGSCALWVSQPPETRTLEGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
Db 1 MAWMLLLILMVHPGSCALWVSQPPETRTLEGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60

QY	61	VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG	120
Db	61	VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG	120
QY	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQK-----CLTWKGP	172
Db	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHGMTHCHSSDGP	180
QY	173	RRLPAVVPAPLPP	186
Db	181	R----GVIPERCP	190
RESULT 5			
ID	ADQ19810	ADQ19810 standard; protein; 190 AA.	
XX	AC	ADQ19810;	
XX	DT	12-AUG-2004 (first entry)	
XX	XX	Human PRO polypeptide #367.	
XX	KW	Human; PRO; immune related disorder; systemic lupus erythematosus;	
XX	KW	rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;	
XX	KW	systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;	
XX	KW	autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;	
XX	KW	diabetes mellitus; renal disease; demyelinating disease;	
XX	KW	central nervous system; peripheral nervous system;	
XX	KW	demyelinating polynuropathy; Guillain-Barre syndrome;	
XX	KW	chronic inflammatory demyelinating polynuropathy.	
XX	OS	Homo sapiens.	
XX	PN	WO2004043361-A2.	
XX	PD	27-MAY-2004.	
XX	PF	06-NOV-2003; 2003WO-US035268.	
XX	PR	08-NOV-2002; 2002US-0425235P.	
XX	PA	(GETH) GENENTECH INC.	
XX	PI	Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;	
XX	PI	Wood WI, Wu TD;	
XX	DR	WPI; 2004-420067/39.	
XX	DR	N-PSDB; ADO19809.	
XX	PT	Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for	
XX	PT	treating an immune related disorder such as systemic lupus erythematosus,	
XX	PT	rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or	
XX	PT	spondyloarthropathy.	
XX	PS	Claim 7; SEQ ID NO 734; 1731pp; English.	
XX	CC	The invention relates to human PRO polypeptides and the polynucleotides	
XX	CC	encoding them. The polypeptides and polynucleotides are useful for	
XX	CC	treating and diagnosing immune related disorders in mammals. The immune	
XX	CC	related disorders include systemic lupus erythematosus, rheumatoid	
XX	CC	arthritis, osteoarthritis, juvenile chronic arthritis, systemic	
XX	CC	sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune	
XX	CC	haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes	
XX	CC	mellitus, immune-mediated renal disease, demyelinating diseases of the	
XX	CC	central or peripheral nervous system, demyelinating polynuropathy,	
XX	CC	Guillain-Barre syndrome and chronic inflammatory demyelinating	
XX	CC	polynuropathy. This sequence represents a human PRO polypeptide of the	
XX	CC	invention.	
XX	CC	Sequence 190 AA;	

Query Match	82.1%;	Score	876;	DB	8;	Length	190;
Best Local Similarity	89.2%;	Pred. No.	5.9e-75;				
Matches	173;	Conservative	2;	Mismatches	7;	Indels	12;
						Gaps	2;
QY	1	MAMMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV	60				
Db	1	MAMMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV	60				
QY	61	VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG	120				
Db	61	VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVRGHDAIYVCRVEVLGLGVGTG	120				
QY	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQK-----CLTWKGP	172				
Db	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHGMTHCHSSDGP	180				
QY	173	RRLPAVVPAPLPP	186				
Db	181	R----GVIPERCP	190				
RESULT 6							
ID	ADQ30923	ADQ30923 standard; protein; 190 AA.					
XX	AC	ADQ30923;					
XX	DT	23-SEP-2004 (first entry)					
XX	XX	Human NKP30 polypeptide.					
XX	KW	Natural killer cell; NK cell; NKP30; cytostatic; antimicrobial.					
XX	OS	Homo sapiens.					
XX	FH	Key					
XX	FT	Region					
XX	FT	/label= Extracellular region					
XX	FT	/note= "Region specifically described in Claim 3"					
XX	FT	Region					
XX	FT	/label					
XX	FT	/note= "Immunogenic peptide specifically described in Claim 3"					
XX	FT	Claim 3"					
XX	FT	Region					
XX	FT	/label= Transmembrane region					
XX	FT	/note= "Region specifically described in Claim 3"					
XX	FT	Region					
XX	FT	/label= Cytoplasmic tail					
XX	FT	/note= "Region specifically described in Claim 3"					
XX	PN	WO2004056392-A1.					
XX	PD	08-JUL-2004.					
XX	PF	22-DEC-2003; 2003WO-EP014716.					
XX	PR	23-DEC-2002; 2002US-0435344P.					
XX	PA	(INNA-) INNATE PHARMA.					
XX	PI	Romagne F, Andre P;					
XX	DR	WPI; 2004-507595/48.					
XX	PT	Pharmaceutical compositions that stimulate proliferation of natural					
XX	PT	killer cells useful for therapy of melanoma, chronic myeloid, and					
XX	PT	leukemia, comprise an anti-natural killer cell receptor antibody and					
XX	PT	interleukins.					
XX	PS	Claim 3; SEQ ID NO 1; 35pp; English.					
XX	CC	The present sequence is that of human NKP30, a 190 amino acid polypeptide					
XX	CC	(about 30 kDa on SDS-PAGE) that is selectively expressed by natural					

CC killer (NK) cells, and particularly by mature NK cells. Claimed
 CC pharmaceutical compositions that have a stimulating effect on the
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
 CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to NKp30 or to a
 CC fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,
 CC when used for daily subcutaneous injection, comprising from 1 mg to 100
 CC mg/kg (body weight) of antibody(ies), and lower than 1 million
 CC units/square meters/day of cytokine(s), are useful for the prevention,
 CC palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute
 CC myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung
 CC adenocarcinoma, neuroblastoma and for antimicrobial prevention,
 CC palliation and therapy (claimed).

XX Sequence 190 AA;

Query Match 82.1%; Score 876; DB 8; Length 190;
 Best Local Similarity 89.2%; Pred. No. 5.9e-75;
 Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFREDEV 60
 DB 1 MAWMLLLILMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFREDEV 60
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSVTVYQKG-----CLTWKGP 172
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSVTVYQKGKCHMGTCHSSDGP 180
 QY 173 RRQLPAVVAPLPP 186
 DB 181 R----GVIPERCP 190

RESULT 7
 AAY06401
 ID AAY06401 standard; protein; 190 AA.

XX AAY06401;
 XX 20-SEP-1999 (first entry)
 XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
 XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
 KW signal transduction; immunomodulator; antiinflammatory;
 KW autoimmune disease; inflammation; gene therapy; diagnosis.
 XX Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..12 /note= "leader peptide"
 FT Protein 13..190 /note= "mature protein"
 FT Modified-site 42 /note= "N-glycosylated"
 FT Modified-site 68 /note= "N-glycosylated"
 FT Modified-site 121 /note= "N-glycosylated"
 FT Domain 139..162 /note= "transmembrane domain"
 FT Peptide 166..190 /note= "alternatively spliced C-terminal end"

PN W09923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

XX N-PSDB; AAX59347.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 2; Page 42; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
 CC identified. The protein is present primarily in the spleen, in lymph
 CC nodes and in germinal centre B cells. It may have immunoregulatory
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
 CC producing BMOG using these transformed host cells are also provided. BMOG
 CC polypeptides can be used for modulating the immune system of a subject or
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it
 CC with a soluble BMOG protein. The nucleic acid can be used for gene
 CC therapy. The protein can also be used to target a toxin, imaging agent or
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 190 AA;

Query Match 81.9%; Score 874; DB 2; Length 190;
 Best Local Similarity 88.7%; Pred. No. 9.1e-75;
 Matches 172; Conservative 3; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFREDEV 60
 DB 1 MAWMLLLILMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFREDEV 60
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSVTVYQKG-----CLTWKGP 172
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSVTVYQKGKCHMGTCHSSDGP 180
 QY 173 RRQLPAVVAPLPP 186
 DB 181 R----GVIPERCP 190

RESULT 8
 AAY06402
 ID AAY06402 standard; protein; 177 AA.

XX AAY06402;

XX 20-SEP-1999 (first entry)

XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.

XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
 KW signal transduction; immunomodulator; antiinflammatory;
 KW autoimmune disease; inflammation; gene therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1. .12
FT /note= "leader peptide"
FT Protein 13. .177
FT /note= "mature protein"
FT Modified-site 42
FT /note= "N-glycosylated"
FT Modified-site 68
FT /note= "N-glycosylated"
FT Modified-site 121
FT /note= "N-glycosylated"
FT Domain 139. .162
FT /note= "transmembrane domain"
FT Peptide 166. .177
FT /note= "alternatively spliced C-terminal end"
XX
XX WO9923867-A2.
XX
XX 20-MAY-1999.
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59348.
XX
XX Novel B-cell myelin oligodendrocyte glycoproteins.
XX
XX Claim 2; Page 43; 43pp; English.
XX

CC This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)
XX
XX SQ Sequence 177 AA;

Query Match 80.5%; Score 859; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFWFRDEV 60
Db 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFWFRDEV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDASIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDASIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165

RESULT 9
ADY16598
ID ADY16598 standard; protein; 177 AA.
XX
XX AC ADY16598;

XX 05-MAY-2005 (first entry)
XX PRO polypeptide SEQ ID NO 2404.
XX
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Antiallergic; ds; gene; diagnosis.
XX Homo sapiens.
XX WO2005016962-A2.
XX 24-FEB-2005.
XX 11-AUG-2004; 2004WO-US026249.
XX 11-AUG-2003; 2003US-0493546P.
XX (GETH) GENENTECH INC.
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX Claim 8; SEQ ID NO 2404; 158pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a DNA encoding a PRO
XX polypeptide.
XX
XX SQ Sequence 177 AA;
Query Match 80.5%; Score 859; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFWFRDEV 60
Db 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFWFRDEV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDASIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDASIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165
RESULT 10
AAE19109
ID AAE19109 standard; protein; 135 AA.
XX
XX AAE19109;
XX
XX 21-MAY-2002 (first entry)
XX Human Nkp30 protein.
XX
XX Human; natural killer cell activating protein; Nkp46; therapy; virucide;
XX viral infection; natural killer cell; NK; Nkp44; imaging agent; cancer;
XX detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; Nkp30.
XX

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OS Homo sapiens.
XX WO200208287-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-IL000664.
XX 20-JUL-2000; 2000IL-00137419.
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX (UYNE ) UNIV BEN-GURION NEGEV.
XX Mandelboim O, Porgador A;
XX WPI; 2002-195870/25.
XX N-PSDB; AAD30466.
XX New targeting complex capable of targeting an active substance to a
XX target cell, comprising a target recognition segment and an active
XX segment, useful for treating pathologies associated with viral infections
XX or cancer.
XX Example 1; Page 108; 113pp; English.
XX The invention relates to compositions and methods for the treatment and
XX detection of a variety of viral infections, by using complex agents
XX comprising the natural killer (NK) cells activating proteins, NKp46 and
XX NKp44 and functional fragments thereof, linked to therapeutic or imaging
XX agents. The complex is useful for treating pathologies associated with
XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein
XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)
XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
XX the imaging and monitoring of cancer. The complex may also be used to
XX detect the presence of abnormal cells in a sample. The antibodies can be
XX used to qualitatively or quantitatively detect the ligand for the
XX complex. The present sequence is human NKp30 protein
XX Sequence 135 AA;
XX
XX Query Match 66.8%; Score 713; DB 5; Length 135;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-59;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAWMLLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTWRDEV 60
XX DB 1 MAWMLLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTWRDEV 60
XX
XX QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
XX DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
XX
XX QY 121 NGTRLVVEKEHPOLG 135
XX DB 121 NGTRLVVEKEHPOLG 135
XX
XX RESULT 11
XX AAEL19110
XX ID AAEL19110 standard; protein; 369 AA.
XX AC AAEL19110;
XX XX
XX 29-AUG-2003 (revised)
XX 21-MAY-2002 (first entry)
XX
XX Human NKp30-IgG fusion protein.
XX Human; natural killer cell activating protein; NKp46; therapy; virucide;
XX viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;
XX detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; IgG;
XX immunoglobulin G; fusion protein.
XX

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OS Homo sapiens.
XX Chimeric.
XX Key Location/Qualifiers
XX Region 1..135
XX Region /note= "Human NKp30"
XX Region 136..369
XX Region /note= "Human IgG"
XX WO200208287-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-IL000664.
XX 20-JUL-2000; 2000IL-00137419.
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX (UYNE ) UNIV BEN-GURION NEGEV.
XX Mandelboim O, Porgador A;
XX WPI; 2002-195870/25.
XX N-PSDB; AAD30467.
XX New targeting complex capable of targeting an active substance to a
XX target cell, comprising a target recognition segment and an active
XX segment, useful for treating pathologies associated with viral infections
XX or cancer.
XX Example 1; Page 108-110; 113pp; English.
XX The invention relates to compositions and methods for the treatment and
XX detection of a variety of viral infections, by using complex agents
XX comprising the natural killer (NK) cells activating proteins, NKp46 and
XX NKp44 and functional fragments thereof, linked to therapeutic or imaging
XX agents. The complex is useful for treating pathologies associated with
XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein
XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)
XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
XX the imaging and monitoring of cancer. The complex may also be used to
XX detect the presence of abnormal cells in a sample. The antibodies can be
XX used to qualitatively or quantitatively detect the ligand for the
XX complex. The present sequence is human NKp30- immunoglobulin G (IgG) Fc
XX region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
XX Sequence 369 AA;
XX
XX Query Match 66.8%; Score 713; DB 5; Length 369;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-59;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAWMLLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTWRDEV 60
XX DB 1 MAWMLLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQGRLAIGSVTWRDEV 60
XX
XX QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
XX DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
XX
XX QY 121 NGTRLVVEKEHPOLG 135
XX DB 121 NGTRLVVEKEHPOLG 135
XX
XX RESULT 12
XX AAEL02771
XX ID AAEL02771 standard; protein; 120 AA.
XX AC AAEL02771;
XX XX
XX 06-AUG-2001 (first entry)
XX

```

DE Human Nkp30 receptor extracellular region sequence.

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
 KW therapy; extracellular region.

XX Homo sapiens.

XX WO200136630-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

XX Novel compound, useful for detection and/or quantifying the presence of
 XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX Claim 1; Fig 7B; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA
 CC molecule which is involved in natural cytotoxicity mediated by natural
 CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor
 CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
 CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
 CC useful for detecting and/or quantifying the presence of NK cells in a
 CC biological sample. The invention also provide kits for detecting and/or
 CC quantifying the presence of NK cells, for the selective removal of NK
 CC cells from a biological sample, for the positive and selective
 CC purification of NK cells from a biological sample and for the in vitro
 CC stimulation of NK cell cytotoxicity. The invention further provides a
 CC pharmaceutical composition which is used as a drug for grafting
 CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
 CC versus tumour (GVT) and especially graft versus leukaemia (GvL), and for
 CC the prevention, palliation and/or therapy of solid or liquid tumours,
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for
 CC identifying Nkp30 natural ligands and allow assessment of the level of
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
 CC comparison of this level to the standard physiological one. Hence Nkp30
 CC antibodies are useful in the diagnosis of tumours or of infection. The
 CC present sequence is the extracellular region of human Nkp30 receptor

XX SQ Sequence 120 AA;

Query Match 59.2%; Score 632; DB 4; Length 120;

Best Local Similarity 100.0%; Pred. No. 5.4e-52;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVPKVRNGTPEFRGLA 78

Db 1 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVPKVRNGTPEFRGLA 60

Qy 79 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

Db 61 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120

RESULT 13

ADQ30924

ID ADQ30924 standard; protein; 120 AA.

XX AC ADQ30924;

XX 23-SEP-2004 (first entry)

XX Human Nkp30 extracellular region.

XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.

XX Homo sapiens.

XX WO2004056392-A1.

XX 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014716.

XX 23-DEC-2002; 2002US-0435344P.

XX (INNA-) INNATE PHARMA.

XX Romagne F, Andre P;

XX WPI; 2004-507595/48.

XX Pharmaceutical compositions that stimulate proliferation of natural
 PT killer cells useful for therapy of melanoma, chronic myeloid, and
 PT leukemia, comprise an anti-natural killer cell receptor antibody and
 PT interleukins.

XX Claim 3; SEQ ID NO 2; 35pp; English.

XX The present sequence is that of the extracellular region of human Nkp30
 CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by
 CC natural killer (NK) cells, and particularly by mature NK cells. Claimed
 CC pharmaceutical compositions that have a stimulating effect on the
 CC proliferation of NK cells comprise an antibody such as an anti-Nkp30
 CC antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
 CC antibody(ies) and cytokine(s) being administered together or separately
 CC to a subject. The anti-Nkp30 antibody is an isolated antibody or its
 CC antigen-binding fragment which specifically binds to Nkp30 or to a
 CC fragment, including the extracellular region, of Nkp30. The
 CC pharmaceutical compositions, when used for daily subcutaneous injection,
 CC comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and
 CC lower than 1 million units/square meters/day of cytokine(s), are useful
 CC for the prevention, palliation and therapy of e.g. melanoma, chronic
 CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
 CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
 CC prevention, palliation and therapy (claimed).

XX SQ Sequence 120 AA;

Query Match 59.2%; Score 632; DB 8; Length 120;

Best Local Similarity 100.0%; Pred. No. 5.4e-52;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVPKVRNGTPEFRGLA 78

Db 1 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVPKVRNGTPEFRGLA 60

Qy 79 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

Db 61 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120

RESULT 14

ADP48750

ID ADP48750 standard; protein; 382 AA.

XX AC ADP48750;

XX 09-SEP-2004 (first entry)

XX Human Nkp30-Fc conjugate protein SEQ ID NO:12.

Result No.	Score	Query Match	Length	DB	ID	Description
1	118	11.1	136	2	B45893	T-cell receptor al
2	117.5	11.0	132	2	A24402	T-cell receptor al
3	117.5	11.0	232	2	S25756	Ig lambda chain -
4	116.5	10.9	223	2	T09536	cytotoxic T-lympho
5	116	10.9	146	2	S28408	T-cell receptor be
6	116	10.9	226	2	A46477	membrane-bound imm
7	115	10.8	223	2	A29063	cytotoxic T-lympho
8	113	10.6	233	2	S25747	Ig lambda chain -
9	110	10.3	223	2	I46696	CTLA-4 precursor -
10	110	10.3	235	2	S25749	Ig lambda chain -
11	107.5	10.1	138	2	C27577	T-cell receptor al
12	106.5	10.0	131	2	D24092	T-cell receptor al
13	106.5	10.0	131	2	E24092	T-cell receptor al
14	106	9.9	132	1	RWMSAV	T-cell receptor al
15	105	9.8	131	2	F45893	T-cell receptor al
16	104.5	9.8	132	2	S09713	Ig lambda chain V
17	103	9.7	129	2	A43692	T-cell receptor al
18	103	9.7	235	2	S14675	Ig lambda chain -
19	102.5	9.6	110	2	B24092	T-cell receptor al
20	101.5	9.5	139	2	S63325	T-cell receptor de
21	101	9.5	120	2	I54487	T-cell receptor al
22	101	9.5	186	2	S08614	cytotoxic T-lympho
23	100.5	9.4	236	2	S25746	Ig lambda chain -
24	100.5	9.4	1694	2	S50065	sialoadhesin - mou
25	100	9.4	110	2	A24092	T-cell receptor al
26	99.5	9.3	271	2	A53268	T-cell receptor al
27	99	9.3	130	2	A31211	T-cell receptor al
28	98.5	9.2	128	2	S24319	Ig lambda chain pr
29	98.5	9.2	152	2	S21826	T-cell receptor be

C:Keywords: T-cell receptor

Broad NC is the number of variables predicted by chance to have a
A;RESIDUES: 1-136 <ISH>
X-Chain references: UNPDB: UNP000011D090 CB-D00011 NTD-C017C10 PDBV-BAA140C1 1-PDB

Query Match 11.0%; Score 117.5; DB 2; Length 132;
Best Local Similarity 30.8%; Pred. No. 0.0039;
Matches 44; Conservative 17; Mismatches 47; Indels 35; Gaps 9;

QY 12 VHPGSCALW-----VSOPPE-IRTEGSSAFPCSFNASQGRLAIGSVTWFRDE 59
DB 3 LHVSLVFLWLQGVSVQKQVQSPESLIIVPEGAMVSLNCSFSDS-----ASQSIWVYQQH 58
QY 60 VVPGKEVR-----NGTPFRGRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYVCRV 112
DB 59 --PGKPKALISIFSGNKK-EGRLTVYLNRAHLH---VSLHIKQSPSDSAVYLCAVRR 112
QY 113 LGLGVGT---GNGTRLVVEKEHP 132
DB 113 SGANTGKLTGCHGTILRV---HP 132

RESULT 3
S25756
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25756
R;Combiarto, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25756
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COW>
A;Cross-references: UNIPARC:UPI0000115F04; EMBL:X57821; NID:g33741; PIDN:CAA40958.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 117.5; DB 2; Length 232;
Best Local Similarity 24.7%; Pred. No. 0.0072;
Matches 53; Conservative 27; Mismatches 74; Indels 61; Gaps 10;

QY 1 MAMLLILIMVH-PGSCALWV-SQPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRD 58
DB 1 MAWTVLLGLLGHCTGTSVTLTPQPSVAPGKTASITCGN---NIGSKSVHWYQQ 56
QY 59 EVVPGK-----EVRNGTPE-FRGRGLAPLASSRFLHDHQAELHIRDVRGHDASIVY 107
DB 57 K--PGQAPVLVYDDSDRPSGIPERFSGNS-----GNTATLTISRVEAGDEADYY 105
QY 108 CHVEVLGLGVGTGNGTRLVW-----EKEHPQLGAGTVLLLRAGFY--AVS 150
DB 106 CQWDSDDVDFGGGKTLVLQPKAAPSVTLPFPSSBELQANKATLVCLISDFYPGAVT 165
QY 151 FLSVAVGSTVYVYQGGKLTWKGPRRLQPAVVPAPLP 185
DB 166 -----VAMKADSPVKAGVETTP 184

RESULT 4
T09536
cytotoxic T-lymphocyte protein 4 - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09536
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mouse
A;Reference number: I49584; MUID:91318145; PMID:1713603
A;Accession: T09536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-223 <HAR>
A;Cross-references: UNIPARC:UPI0000113991; EMBL:L15006; NID:g291928; PIDN:AAE59385.1; PI
C;Genetics:

A;Gene: CTLA4
A;Map position: 2q33
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C;Keywords: T-cell; transmembrane protein

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0084;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

QY 6 LLILIMVHGSC-ALWVSQPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGK 64
DB 24 LLFLLFIIVFCCKMEVQPAVVLASSRGIASFVCEY-ASPGKATVRVTVLQADSQVT 82
QY 65 EVRNGTPEFRGRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIVYVCRV 113
DB 83 EVCAATYMGNELT-----FLDDSICTGSSGNQVNLITQGLRAMDTGLYICKVELMYP 136
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLR-----GFVAVSFLSVAVGSTVYVYQKCLT 168
DB 137 PPVYLGIGNGTQIYVIDPEPCPDSDLMLLAAVSSGLFFYSFLTAVSLS-----KMLK 191
QY 169 WKPRRLQPAVVPAPLP 188
DB 192 KRSPLTTGTVVYKMPTEPEC 211

RESULT 5
S26408
T-cell receptor beta chain V region (5.5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26408
R;Bowman, S.J.; Lanchbury, J.S.
submitted to the EMBL Data Library, September 1992
A;Description: T cell receptor beta chain sequences from patients with rheumatoid arthri
A;Reference number: S26408
A;Accession: S26408
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <BOW>
A;Cross-references: UNIPARC:UPI00001160F7; EMBL:X68527; NID:g36172; PIDN:CAA48540.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-112/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 116; DB 2; Length 146;
Best Local Similarity 26.5%; Pred. No. 0.0058;
Matches 39; Conservative 26; Mismatches 52; Indels 30; Gaps 7;

QY 1 MAMLLILIMVH-PGSCALWVSQPE-IRTEGSSAFPCSFNASQGRLAIGSVTWFRD 58
DB 6 LCWVLLCLL---GAGSVETGVTQSPTHLIKT-RGQVTLRCSQSGH-----NTVSWYQQ 56
QY 59 EVVPG-----KEVRNGTPEFRGRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYVCRV 110
DB 57 ALGQGPQPIFOYREENG-----RGNFPFRSGLOFPNYSSELNVNLELDDSDALYLCA 112
QY 111 EVLGLGVGT-----GNGTRLVVEKE 130
DB 113 SFKGLGLPSRGVEYFGPGTTLTVTED 139

RESULT 6
A46477
membrane-bound immunoglobulin Ig-alpha chain precursor - human
N;Alternate names: B-cell antigen receptor complex alpha chain CD79a; IgM-alpha; immunog
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: I54539; A46477; A49135; A46479; I54496; I57851; S51113
R;Hashimoto, S.; Mohrenweiser, H.W.; Gregersen, P.K.; Chlorazzi, N.
Immunogenetics 40, 287-295, 1994
A;Title: Chromosomal localization, genomic structure, and allelic polymorphism of the hu
A;Reference number: I54539; MUID:94364636; PMID:7916003

Query Match 10.9%; Score 116; DB 2; Length 226;

RESULT 8
S25747
Ig lambda

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25747
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A;Reference number: S16439; MUID:91257162; PMID:1904362
C;Accession: S25747
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: UNIPARC:UPI0000115BFB; EMBL:X57812; NID:G33723; PIDN:CAA40949.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 10.6%; Score 113; DB 2; Length 233;
Best Local Similarity 26.0%; Pred. No. 0.018;
Matches 56; Conservative 27; Mismatches 72; Indels 60; Gaps 12;
QY 1 MAWMLLLIIMVH-PGSCALWV-SOPPEIRTELGSSAPLPCSFNASQ-RLAIGSVTWFR 57
DB 1 MAWVLLGLLCHTGVSTVLTQPPSVVAPGAARITCG-----GINTASKSVHWYQ 55
QY 58 DE-----VVPQKEVR-NGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDASIVC 108
DB 56 KQPGQAPVLVYGSDRPSGIPERFSGNS-----GNTATLINISRVGAEDEAAYC 106
QY 109 RV-EVLGLCVGTNGTRLV-----EKEHPQLGAGTVLLLRAGFY--AVS 150
DB 107 QWDSSSHVYVFGGTKLTVLQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVT 166
QY 151 FLSVAVGTVVYVYQKCLTWKGRQLPAVVPAPLP 185
DB 167 -----VAKKADSSPVKAGVETTP 185

RESULT 9
146696
CTLA-4 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146696
R;Isiono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A;Reference number: 146689; MUID:95369849; PMID:7642234
A;Accession: 146696
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-223 <ISO>
A;Cross-references: UNIPROT:P42072; UNIPARC:UPI000012862A; GB:D49844; NID:G755100; PIDN:
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match 10.3%; Score 110; DB 2; Length 223;
Best Local Similarity 26.9%; Pred. No. 0.031;
Matches 52; Conservative 24; Mismatches 101; Indels 16; Gaps 5;
QY 6 LLILIMVHPCALWV-SOPPEIRTELGSSAPLPCSFNASQRLAIGSVTWFRDEVVPQKE 65
DB 25 LFSLLFLVFSKALHVSQPAVLLASSRGVASFVCEY-ASSHKATEVTVLRLQANSQMT 83
QY 66 VRNGTPEFRGLAPLASSR---FLHDHQAELHIRDVRGHDASIVYCRVEVL---GLGVGT 119
DB 84 VCAMTYTVENELTFIDSTCTGISHGNKNVLTIOGLSAMDTGLYICKVELMYPPPYVGM 143
QY 120 GNGTRLVVEKHPQLGAGTVLLRA---GPIYAVSFLSVAVGTVVYVYQKCLTWKGRPRQ 175
DB 144 GNGTQIVIEPEPCPSDFLLWILAAISSGLFFYSFLITAVLSL-----KMLKKRSPLTT 198
QY 176 LPAVVPAPLP 188
DB 199 GVIYKMPTEPEC 211

RESULT 10

S25749
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25749
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A;Reference number: S16439; MUID:91257162; PMID:1904362
C;Accession: S25749
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: UNIPARC:UPI0000115BFD; EMBL:X57814; NID:G33727; PIDN:CAA40951.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match 10.3%; Score 110; DB 2; Length 235;
Best Local Similarity 23.7%; Pred. No. 0.032;
Matches 52; Conservative 29; Mismatches 72; Indels 66; Gaps 12;
QY 1 MAWMLLLIIMVHPS---CALWVSQPPPEIRTELGSSAPLPCSFNASQRLAIGSVTWFR 57
DB 1 MAWMLLLGLLAY-GSGVDSQTVVTOEPSFMSPGGTVLTTCGLSSGSGSTSY-SPSWYQ 58
QY 58 DEVVPQKEVR-----NGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDASIV 106
DB 59 Q--TPQAPRTLMYNTNRSSGVPDRFSGSIL-----GNKSALTITGAQAEESDY 107
QY 107 VCRVEVLGLGVGT---GNGTRLV-----EKEHPQLGAGTVLLLRAGFY- 147
DB 108 YC---VLYMGRGIVIFGGTKLTVLQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYP 164
QY 148 -AVSFLSVAVGTVVYVYQKCLTWKGRQLPAVVPAPLP 185
DB 165 GAVT-----VAKKADSSPVKAGVETTP 187

RESULT 11

C27577
T-cell receptor alpha chain V region (5/10-20D) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C;Accession: C27577; C27557
R;Iwamoto, A.; Ohashi, P.S.; Pircher, H.; Walker, C.L.; Michalopoulos, E.E.; Rupp, F.; H
J. Exp. Med. 165, 591-600, 1987
A;Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. Pr
A;Reference number: A27557; MUID:87139812; PMID:3493320
A;Accession: C27577
A;Molecule type: mRNA
A;Residues: 1-138 <IWA>
A;Cross-references: UNIPARC:UPI00001768DB
A;Accession: C27557
A;Molecule type: mRNA
A;Residues: 22-138 <IW2>
A;Cross-references: UNIPARC:UPI00001768DB; EMBL:X05733
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.1%; Score 107.5; DB 2; Length 138;
Best Local Similarity 31.9%; Pred. No. 0.03;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;
QY 21 VSQPPPE-IRTELGSSAPLPCSFNASQRLAIGSVTWFRDEVVPQKEVR-----NGTPE 72
DB 24 VQSPESLIVPEGAMTSLNCTFSDSASQY----FAWYRQH--SGKAPKALMSIFSGEKE 77
QY 73 FRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVL-GLGVGTNGTRLVVEKE 130

Db 78 -EGRFTIHLNKASLH---FSLHIRDSQPSDSALYLCAVSMGKYKVFSGTRLLVSPD 132

RESULT 12

D24092

T-cell receptor alpha chain precursor V region (B10) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 01-Dec-2000 #text_change 11-Jan-2002

C:Accession: D24092; S03507

R:Finck, P.J.; Mattis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.

Nature 321, 219-226, 1986

A:Title: Correlations between T-cell specificity and the structure of the antigen receptor

A:Reference number: A93380; MUID:86230843; PMID:3012351

A:Accession: E24092

A:Molecule type: mRNA

A:Residues: 1-131 <FIN>

A:Cross-references: UNIPARC:UPI0000176EBD

R:Wimoto, A.; Mjolaness, S.; Hood, L.

Nature 316, 832-836, 1985

A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.

A:Reference number: S03503; MUID:85296332; PMID:2993908

A:Accession: S03507

A:Molecule type: DNA

A:Residues: 111-130 <WIN>

A:Cross-references: UNIPARC:UPI0000115274; EMBL:X03057; NID:G54519; PIDN:CAA26864.1; PIDN:CAA26864.1; PIDN:CAA26864.1

A:Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <MAT>

F:36-109/Domain: immunoglobulin homology <IMW>

Query Match 10.0%; Score 106.5; DB 2; Length 131;

Best Local Similarity 29.6%; Pred. No. 0.034;

Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

Qy 21 VSQPEIRTL-EGSAFLPCSFNASQGLAIGSVTWTF----RDEVVPGKEVRNGTPPERG 75

Db 24 VEQSPSALSLEHGTSALRCNFTTT-----MRAVQWFRKNGSLINLFYLSAGTK-NG 77

Qy 76 RLAPLASSRFLHDHQAELHIRDVGRGHDASIIYVCRVEVLGLGVGTGNGTRLVVVEKEHPOLG 135

Db 78 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAE-----ATSSGOKLV-----FG 121

Qy 136 AGTVL 140

Db 122 QGTIL 126

RESULT 13

E24092

T-cell receptor alpha chain precursor V region (4.C3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000

C:Accession: E24092

R:Finck, P.J.; Mattis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.

Nature 321, 219-226, 1986

A:Title: Correlations between T-cell specificity and the structure of the antigen receptor

A:Reference number: A93380; MUID:86230843; PMID:3012351

A:Accession: E24092

A:Molecule type: mRNA

A:Residues: 1-131 <FIN>

A:Cross-references: UNIPARC:UPI0000176E34

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <MAT>

F:36-109/Domain: immunoglobulin homology <IMW>

Query Match 10.0%; Score 106.5; DB 2; Length 131;

Best Local Similarity 29.6%; Pred. No. 0.034;

Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

Qy 21 VSQPEIRTL-EGSAFLPCSFNASQGLAIGSVTWTF----RDEVVPGKEVRNGTPPERG 75

Db 24 VEQSPSALSLEHGTSALRCNFTTT-----MRAVQWFRKNGSLINLFYLSAGTK-NG 77

Qy 76 RLAPLASSRFLHDHQAELHIRDVGRGHDASIIYVCRVEVLGLGVGTGNGTRLVVVEKEHPOLG 135

Db 78 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAE-----STSSGOKLV-----FG 121

Qy 136 AGTVL 140

Db 122 QGTIL 126

RESULT 14

RWMSAV

T-cell receptor alpha chain precursor V region (2B4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A02015

R:Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.

Nature 312, 31-35, 1984

A:Title: A third type of murine T-cell receptor gene.

A:Reference number: A93344; MUID:85036634; PMID:6548551

A:Accession: A02015

A:Molecule type: mRNA

A:Residues: 1-132 <CHI>

A:Cross-references: UNIPROT:P01739; UNIPARC:UPI00000270CC

A:Experimental source: hybridoma 2B4, clone TT11

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: Glycoprotein; heterotrimer; receptor; T-cell

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <MAT>

F:21-113/Region: V segment

F:114-117/Region: D segment

F:118-132/Region: J segment

F:42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 106; DB 1; Length 132;

Best Local Similarity 25.8%; Pred. No. 0.038;

Matches 40; Conservative 22; Mismatches 45; Indels 48; Gaps 9;

Qy 3 WMLLLILIMVHGPSALWVS-----OPPEIRTEGSSAFPCSFNASQGLAIGSVTW 55

Db 12 WLLIL-----NWVNSQNVQSPESLIIVPEGARTSLNCTFSDASQY----FWW 55

Qy 56 FRDEVVPGKEVR-----NGTPEFRGLAPLASSRFLHDHQAELHIRDVGRGHDASIIYV 108

Db 56 YRQH--SGKAPKALMSIFSNKEKE-EGRTIHLNKASLH---FSLHIRDSQPSDSALYLC 109

Qy 109 RVEVLGLGVGTGNGTRLVVVEKEHPOLGAGTVLLLR 143

Db 110 AVTIYG-----GSGNKLI-----FGTGILLSVK 132

RESULT 15

F45893

T-cell receptor alpha chain precursor V region (BTA25) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000

C:Accession: F45893

R:Ishiguro, N.; Tanaka, A.; Shinagawa, M.

Immunogenetics 31, 57-60, 1990

A:Title: Sequence analysis of bovine T-cell receptor alpha chain.

A:Reference number: A45893; MUID:90129157; PMID:2137108

A:Accession: F45893

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <ISH>

A:Cross-references: UNIPARC:UPI000011D08D; GB:D90015; NID:G217618; PIDN:BAAL4065.1; PIDN:BAAL4065.1; PIDN:BAAL4065.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:36-109/Domain: immunoglobulin homology <IMW>

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
OM protein - protein search, using sw model
Run on: February 27, 2006, 17:56:08 ; Search time 230 Seconds
(without alignments)
616.570 Million cell updates/sec
Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWMLLLILIMVHFGSCALW.....APLPPPCGSSAHLPPVPG 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1067	100.0	201	1	NCTR3_HUMAN
2	1051	98.5	201	1	NCTR3_PANTR
3	1018	95.4	201	1	NCTR3_MACMU
4	826	77.4	176	1	NCTR3_MACFA
5	590	55.3	192	1	NCTR3_RAT
6	504	47.2	122	2	Q4ZJ77_CANFA
7	136.5	12.8	235	2	Q99M11_MOUSE
8	126	11.8	221	2	Q28090_BOVIN
9	124	11.6	221	2	Q97631_SHEEP
10	123.5	11.6	313	2	Q6IPU1_HUMAN
11	122.5	11.5	234	2	Q6GMW3_HUMAN
12	121	11.3	223	2	Q7TMX1_MOUSE
13	119	11.2	223	2	Q7JHU0_MACNE
14	119	11.2	223	2	Q7JHU2_CERTO
15	119	11.2	223	2	Q9BDC4_MACMU
16	119	11.2	223	2	Q9BDN7_PAPAN
17	118.5	11.1	223	1	CTLA4_HUMAN
18	118.5	11.1	223	2	Q33T05_HUMAN
19	118.5	11.1	223	2	Q6GR94_HUMAN
20	118	11.1	223	2	Q62859_RAT
21	117	11.0	223	2	Q6GTR6_MOUSE
22	116	10.9	226	1	CTD9A_HUMAN
23	115	10.8	223	1	CTLA4_MOUSE
24	115	10.8	223	2	Q9GKP2_CANFA
25	112.5	10.5	234	2	Q6GMV8_HUMAN
26	112	10.5	223	2	Q9XSY7_FELCA
27	112	10.5	223	2	Q9XTAL_FELCA
28	112	10.5	700	1	K1RR2_MOUSE
29	111	10.4	223	2	Q9JLV3_MARMO
30	110	10.3	223	1	CTLA4_FIG
31	110	10.3	223	1	CTLA4_RABIT

32	110	10.3	223	2	Q9N186_PIG	Q9N186 sus scrofa
33	110	10.3	233	2	Q96I69_HUMAN	Q96I69 homo sapien
34	110	10.3	237	2	Q6DHW4_HUMAN	Q6DHW4 homo sapien
35	109.5	10.3	240	2	Q6MG96_RAT	Q6MG96 rattus norv
36	109	10.2	172	2	Q71AW3_BOVIN	Q71aw3 bos taurus
37	109	10.2	223	2	Q9BDP1_AOTTR	Q9bdp1 actus trivi
38	108.5	10.2	236	2	Q6GMX4_HUMAN	Q6gmX4 homo sapien
39	108.5	10.2	350	2	Q9VFU7_DROME	Q9vfU7 drosophila
40	108.5	10.2	449	2	Q9NKA5_DROME	Q9nka5 drosophila
41	108.5	10.2	867	2	Q59DZ1_DROME	Q59dz1 drosophila
42	108	10.1	387	1	SIG13_PANTR	Q64ja4 pan troglod
43	107	10.0	226	2	Q53F88_HUMAN	Q53fb8 homo sapien
44	106.5	10.0	236	2	Q6PI07_HUMAN	Q6pi07 homo sapien
45	106	9.9	132	1	TV2A_MOUSE	P01739 mus musculu

ALIGNMENTS

RESULT 1

NCTR3_HUMAN STANDARD; PRT: 201 AA.

AC O14931; O14930; O14932; O95667; O95668; O95669; Q5ST90; Q5ST91; Q5ST92; Q5STA3;

DT 05-JUL-2004 (Rel. 44, Created)

DT 13-SEP-2005 (Rel. 48, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (Nkp30) (NK-p30).

DE Name=NCR3; Synonyms=IC7;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH CD3Z, AND FUNCTION.

RC TISSUE=Lymphoid;

RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R., Morelli L., Marcenaro E., Accame L., Malaespina A., Biassoni R., Bottino C., Moretta L., Moretta A.;

RA "Identification and molecular characterization of Nkp30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells."

RL J. Exp. Med. 190:1505-1516(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION WITH CD3Z.

RC TISSUE=Peripheral blood;

RA Sato M., Yabe T., Ohaehi J., Teuchiya N., Hanaoka K., Tokunaga K., Juji T.;

RA "Identification of two novel single nucleotide polymorphisms in the Nkp30 gene in human natural killer cells."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5 AND 6).

RC MEDLINE=99218514; PubMed=10202016;

RA Neville M.J., Campbell R.D.;

RA "A new member of the Ig superfamily and a V-ATPase G subunit are among the predicted products of novel genes close to the TNF locus in the human MHC."

RL J. Immunol. 162:4745-4754(1999).

RN [4]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).

RC TISSUE=Spleen;

RA MEDLINE=96422187; PubMed=8824804; DOI=10.1006/geno.1996.0034;

RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;

RA "Genes in a 220-kb region spanning the TNF cluster in human MHC."

RL Genomics 31:215-222(1996).

RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=1465967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.,
RT "Analysis of the gene-dense major histocompatibility complex class III
RT region and its comparison to mouse";
RL Genome Res. 13:2621-2636(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Shijina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of Sp21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Culley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Laylor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McClann O.T., McLaren S.J., McLeay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon I.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sultston J.E., Dunham I., Rogers J., Beck S.;
RT "The DNA sequence and analysis of human chromosome 6";
RL Nature 425:805-811(2003).
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Blood.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).


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DR EMBL; BC052582; AAH52582.1; -: mRNA.
DR HGNC; HGNC:19077; NCR3.

Query Match      100.0%; Score 1067; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMLLILIMVHPGSCALWVSQPPEIRTLLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
Db 1 MAMMLLILIMVHPGSCALWVSQPPEIRTLLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
Qy 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120
Db 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCLTWKGPRLPAVV 180
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCLTWKGPRLPAVV 180
Qy 181 PAPLPPPCGSSAHLPPVPGG 201
Db 181 PAPLPPPCGSSAHLPPVPGG 201

RESULT 2
NCTR3_PANTR
ID NCTR3_PANTR STANDARD; PRT; 201 AA.
AC P61484;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Natural cytotoxicity activating receptor 3 precursor (Natural killer
DE cell p30-related protein) (Nkp30) (NK-p30).
GN Name=NCR3;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OC NCBI_TaxID=9598;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymphoid;
RA Blassoni R.;
RT "Characterization of natural killer receptors in chimpanzees.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -1- SUBUNIT: Interacts with CD32 (By similarity).
CC -1- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)
CC family.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ516006; CAD56759.1; -: mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
FT SIGNAL 1 18
FT CHAIN 19 201 Natural cytotoxicity triggering receptor
FT FT 3.
FT TOPO_DOM 19 135 Extracellular (Potential).
FT TRANSMEM 136 156 Potential.
FT TOPO_DOM 157 201 Cytoplasmic (Potential).
FT DOMAIN 19 126 Ig-like.

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FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
FT DISULFID 39 108 By similarity.
SQ SEQUENCE 201 AA; 21656 MW; 3768ACCT68B8D749 CRC64;

Query Match      98.5%; Score 1051; DB 1; Length 201;
Best Local Similarity 99.0%; Pred. No. 3.7e-82;
Matches 199; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MAMMLLILIMVHPGSCALWVSQPPEIRTLLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
Db 1 MAMMLLILIMVHPGSCALWVSQPPEIRTLLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
Qy 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120
Db 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCLTWKGPRLPAVV 180
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCLTWKGPRLPAVV 180
Qy 181 PAPLPPPCGSSAHLPPVPGG 201
Db 181 PAPLPPPCGSSAHLPPVPGG 201

RESULT 3
NCTR3_MACMU
ID NCTR3_MACMU STANDARD; PRT; 201 AA.
AC Q8MJ02; Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;
DT 05-JUL-2004 (Rel. 44, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer
DE cell p30-related protein) (Nkp30) (NK-p30).
GN Name=NCR3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
OX [1]
RN NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.
RA LaBonte M.L., Miller J., Letwin N.L.;
RT "Molecular cloning of rhesus monkey Nkp46 and Nkp30 and identification
RT of Nkp46SD and Nkp30S.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 4), AND VARIANT VAL-156.
RC TISSUE=Lymphoid;
RA Rizzi M., Blassoni R.;
RT "NCR express by macaca NK cells.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 5).
RP PubMed=15269276; DOI=10.1093/molbev/msh216;
RA Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT "Rhesus macaque class I duplicon structures, organization, and
RT evolution within the alpha block of the major histocompatibility
RT complex.";
RL Mol. Biol. Evol. 21:2079-2091(2004).
CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -1- SUBUNIT: Interacts with CD32 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=5;
CC IsoId=Q8MJ02-5; Sequence=Displayed;
CC Name=1;
CC IsoId=Q8MJ02-1; Sequence=VSP_013641, VSP_013642;
CC Note=No experimental confirmation available;

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CC	Name=2;	
CC	Isoid=Q8MJ02-2; Sequence=VSP_010414;	
CC	Notes=No experimental confirmation available;	
CC	Name=3;	
CC	Isoid=Q8MJ02-3; Sequence=VSP_010415, VSP_010416;	
CC	Notes=No experimental confirmation available;	
CC	Name=4;	
CC	Isoid=Q8MJ02-4; Sequence=VSP_010417;	
CC	Notes=No experimental confirmation available;	
CC	-1- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR) family.	
CC	-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	
CC	EMBL; AY035214; AAK63116.1; -; mRNA.	
DR	EMBL; AY035215; AAK63117.1; -; mRNA.	
DR	EMBL; AY035216; AAK63118.1; -; mRNA.	
DR	EMBL; AY035217; AAK63119.1; -; mRNA.	
DR	EMBL; AJ254301; CAD86942.1; -; mRNA.	
DR	EMBL; AB128049; BAD69721.1; -; Genomic_DNA.	
DR	HSSP; P16410; 1185.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	SMART; SM00409; IG; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
KW	Alternative splicing; Glycoprotein; Immunoglobulin domain;	
KW	Polymorphism; Receptor; Signal; Transmembrane.	
FT	SIGNAL 1	Potential.
FT	CHAIN 19 201	Natural cytotoxicity triggering receptor
FT	TOPO DOM 19 133	3.
FT	TRANSMEM 134 154	Extracellular (Potential).
FT	TOPO DOM 155 201	Potential.
FT	DOMAIN 19 126	Cytoplasmic (Potential).
FT	CARBOHYD 42 42	Ig-like.
FT	CARBOHYD 121 121	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID 39 108	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC 66 90	By similarity.
FT	VARSPLIC 112 115	Missing (in isoform 2).
FT	VARSPLIC 116 201	/FTID=VSP_010414.
FT	VARSPLIC 167 180	VLGL -> NILS (in isoform 3).
FT	VARSPLIC 177 201	/FTID=VSP_010415.
FT	VARSPLIC 181 201	Missing (in isoform 3).
FT	VARIANT 156 156	/FTID=VSP_010416.
FT	SEQUENCE 201 AA; 21684 MW; AE3A325C8585BA68 CRC64;	Missing (in isoform 1).
FT		isoform 1).
FT		/FTID=VSP_013641.
FT		Missing (in isoform 4).
FT		/FTID=VSP_010417.
FT		Missing (in isoform 1).
FT		/FTID=VSP_013642.
FT		M -> V.
SQ		
QY	Query Match	
Db	Best Local Similarity 95.0%; Score 1018; DB 1; Length 201;	
QY	Matches 191; Conservative	
Db		
QY	1 MAWMLLLILIMVHPGSCALWVSPPEIRLTGSSAFPLCSFNASQRLAIGSVTWFRDEV 60	
Db	1 MAWMLLLILIMVHPGSCALWVSPPEIRLTGSSAFPLCSFNASQRLAIGSVTWFRDEV 60	
QY	61 VPQKEVRNGTPEPRGRILAPLASSRFLHDQAEHLHIDVRGHDAISYVCREVLGLGVGTG 120	
Db	61 APQKEVRNGTPEPRGRILAPLASSRFLHDQAEHLHIDVRGHDAISYVCREVLGLGVGTG 120	
QY	121 NGTRLVVEKEHPDGLAGTAVLLIRAGFVVSFLSVAVGSTVYVYQKCLTWKGRRLQPAVV 180	
Db	121 NGTRLVVEKEHPDGLAGTAVLLIRAGFVVSFLSVAVGSTVYVYQKCLTWKGRRLQPAVV 180	

Qy 121 NGTRLVVEKEHPQLGAGTGLVLLLRAGFYAVSFLSVAVGTVVYQK 166
Db 121 NGTRLVVEKEYPQLGAGTGLVLLLRAGFYAVSFLSVAVGTVVYQK 166

RESULT 5
NCTR3 RAT STANDARD; PRT; 192 AA.
AC Q8CFD9; Q80WM8; Q8CG11;
05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).
GN Name=Ncr3; Synonyms=1c7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN NUCLEOTIDE SEQUENCE, AND VARIANTS VAL-7; VAL-19; VAL-82 AND THR-138.
RP STRAIN=PVG; TISSUE=Natural killer cell;
RC PubMed=12548565; DOI=10.1002/immu.200310008;
RX Backman-Petersson E., Miller J.R., Hollyoake M., Aguado B., Butcher G.W.;
RA "Molecular characterization of the novel rat NK receptor 1c7.";
RL Eur. J. Immunol. 33:342-351(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Lewis;
RX MEDLINE=22168131; PubMed=12180816; DOI=10.1016/S0966-3274(02)00033-3;
RA Heish C.L., Obara H., Ogura Y., Martinez O.M., Krams S.M.;
RL "NK cells and transplantation.";
RN Transpl. Immunol. 9:111-114(2002).
[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Brown Norway;
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T., Inoko H., Leirach H., Guenther E., Reinhardt R., Himmelbauer H.;
RL "The genomic sequence and comparative analysis of the rat major histocompatibility complex.";
RT Genome Res. 14:631-639(2004).
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC ENBL; AJ430418; CAD23066.1; -; mRNA.
CC ENBL; AJ430419; CAD23067.2; -; Genomic DNA.
CC ENBL; AJ430420; CAD23067.2; JOINED; Genomic DNA.
CC ENBL; AY273824; AAP13457.1; -; mRNA.
CC ENBL; BX883046; CAE84000.1; -; Genomic DNA.
CC HSSP; P09793.1DQT.
CC Ensembl; ENSRNOG0000000854; Rattus norvegicus.
CC RGD; 727881; 1c7.
CC InterPro; IPR003599; Ig.
CC SMART; SM00409; Ig-like.
CC PROSITE; PS00835; IG-LIKE; 1.
CC Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;

Transmembrane. 18 Potential.
FT SIGNAL 192 Natural cytotoxicity triggering receptor 3.
FT CHAIN 192
FT
FT TOPO_DOM 19 147 Extracellular (Potential).
FT TRANSMEM 148 168 Potential.
FT TOPO_DOM 169 192 Cytoplasmic (Potential).
FT DOMAIN 19 126 Ig-like.
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
FT DISULFID 39 108 By similarity.
FT VARIANT 7 7 I -> V.
FT VARIANT 19 19 I -> V.
FT VARIANT 82 82 A -> V.
FT VARIANT 138 138 A -> T.
FT CONFLICT 135 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB252D2377 CRC64;
Query Match 55.3%; Score 590; DB 1; Length 192;
Best Local Similarity 64.2%; Pred. No. 1.3e-42;
Matches 115; Conservative 24; Mismatches 32; Indels 8; Gaps 1;
Qy 1 MAMWLLILLVHPGSCALWVOPPEIRTLGGSSAFPCSFNASQGRLAIGSVTFPRDEV 60
Db 1 MAKVLLIVFTVYAGSCAIWVOPPEIRTAQEGTTASLPCSFNASRGAATGYQDKV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120
Db 61 AFGWELSNVTPGFRGRVASFASQFIRGHKAGLLIQIDQSHDARIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQ-----LGATVLLLRAGFYAVSFLSVAVGTVVYQKCLTWKG 171
Db 121 NGTRLVVEKEPPQQAASNAEPAAYTSLLRAGYVALSFLSVATGTVYVYQKCLCHVG 179
RESULT 6
Q4ZJE7 CANFA
ID Q4ZJE7 CANFA PRELIMINARY; PRT; 122 AA.
AC Q4ZJE7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE NKp30 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; DQ003484; AY21817.1; -; mRNA.
FT NON_TER 122 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13307 MW; FB14BD6B314279DA CRC64;
Query Match 47.2%; Score 504; DB 2; Length 122;
Best Local Similarity 79.5%; Pred. No. 2e-35;
Matches 97; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
Qy 19 LWVSQPPPEIRTLGGSSAFPCSFNASQGRLAIGSVTFPRDEVVPGKEVRNGTPEFRGLA 78
Db 1 LWVFPPEIHTQGTAAFLPCSFNASERKLAIGSVTYWRDKVAPGKEVRNGTPEFRGLA 60
Qy 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138
Db 61 PLPSSRFLCDHQAELHIWDIQDCDAGVYVCRVEVLGLGVGTGNGTLLVVEKSPWLCAST 120
Qy 139 VL 140
Db 121 VL 122

Db	112	SYSSGIRV-FGGTKLTV	128
RESULT 8			
Q28090	BOVIN	PRELIMINARY;	PRT; 221 AA.
ID	Q28090	BOVIN	PRELIMINARY;
AC	Q28090		
DT	01-NOV-1996	(TRENBLrel. 01, Created)	
DT	01-NOV-1996	(TRENBLrel. 01, Last sequence update)	
DE	01-OCT-2003	(TRENBLrel. 25, Last annotation update)	
DE	CTLA-4	protein precursor.	
GN	Name=CTLA-4;		
OS	Bos taurus	(Bovine).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;		
OC	Pecora; Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=86186531; PubMed=8606060; DOI=10.1007/s002510050080;		
RA	Parsons K.R., Young J.R., Collins R.A., Howard C.J.;		
RT	"cattle CTLA-4, CD28 and chicken CD28 bind CD86: MYPPY is not		
RT	conserved in cattle CD28.";		
RL	Immunogenetics 43:388-391(1996).		
DR	EMBL; X93305; CAA63708.1; -; mRNA.		
DR	HSSP; P16410; I185.		
DR	SMR; Q28090; 35-159.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR008096; CTLA4.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	Pfam; PF00047; ig; 1.		
DR	PRINTS; PR01720; CTLANTIGEN4.		
DR	SMART; SM00409; IG, 1.		
DR	PROSITE; PS00835; IG_LIKE; 1.		
KW	Immunoglobulin domain; Signal.		
FT	SIGNAL 1 35 potential.		
SQ	SEQUENCE 221 AA; 24433 MW; 2CAFL48422C597AA CRC64;		
Query Match	11.8%;	Score 126; DB 2; Length 221;	
Best Local Similarity	27.5%;	Pred. No. 0.011;	
Matches	53; Conservative	26; Mismatches	98; Indels 16; Gaps 5;
Qy	6	LLILIMVHPSGSCALWVSQPPPEIRTEGSSAFPCSFNASQGRLAIGSVTFWREVPQKE	65
Db	23	LFELVFPVFSKGNVTQPPVLAASSRGVASFCEYESS-GKADENVRTVLRAGSQVTE	81
Qy	66	VRNGTPEFRGRRLAPLASSRFL---HDHQAELHIRDVRGHDASIVYCRVEVL---GLGVGT	119
Db	82	VCAGTYMVEDELTFDDSTCTGTSRGNKVNLTIGQLRAMDTGLYVCKVELMYPYPPYVGI	141
Qy	120	GNQTRLVVEXEHPQLGAGTAVLLRA---GFYAVSFSLVAVGTVVYQGGKCLTWKGRRQ	175
Db	142	GNQTYIYVIDPEPCDSDFLWILAVSSGLFFSFILITAVLSL-----KWLKRSPLTT	196
Qy	176	LPAYVPAPLPDPPC	188
Db	197	GVYVKMPTEPEC	209
RESULT 9			
O97631	SHEEP	PRELIMINARY;	PRT; 221 AA.
ID	O97631	SHEEP	PRELIMINARY;
AC	O97631		
DT	01-MAY-1999	(TRENBLrel. 10, Created)	
DT	01-MAY-1999	(TRENBLrel. 10, Last sequence update)	
DE	01-OCT-2003	(TRENBLrel. 25, Last annotation update)	
DE	Cytotoxic T-lymphocyte-associated protein 4.		
GN	Name=CTLA-4;		
OS	Ovis aries	(Sheep).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;		

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OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9309828; PubMed=10380709; DOI=10.1007/s002510050542;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
CC -!- FUNCTION: Not known (By similarity).
CC -!- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By similarity).
CC EMBL; AF092740; AAD04380.1; -; mRNA.
DR HSSP; P16410; 1185.
DR SMR; O97631; 35-159.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 221 AA; 24490 MW; D317B9D5557BA6FB CRC64;

Query Match 11.6%; Score 124; DB 2; Length 221;
Best Local Similarity 26.9%; Pred. No. 0.016;
Matches 52; Conservative 27; Mismatches 98; Indels 16; Gaps 5;

Qy 6 LLILIMVHPGSCALVWSQPPPIRTLGSSAFPCSFNASQGRLAIGSVTWFRDVPKGE 65
Db 23 LFFLLFPVFSKGNVTPPPVVLASSRGVASFCTCEYESS-GKADDEVRTVILRKAGIQVTE 81
Qy 66 VRNGTPEFRGRGLAPLASSRFL---HDHQAELHIRDVRGHDAIYVCRVEVL---GLGVGT 119
Db 82 VCAGTYVVEDELTDSSCGTSGRKNKVNLTIOGLRAMDTGLYVCKVELMYPPTYNGE 141
Qy 120 GNGTRLVVEKHPQLGAGTVLLRA----GFYAVSFSLVAVGSTVYVYQGKCLTWKGRPRQ 175
Db 142 GNGTQIVVIDPEPCPDSDLWILAAVSSGLFFYSFLITAVSLS-----KMLKRSPLTT 196
Qy 176 LPVVPAPLPPEC 188
Db 197 GVYVMPPTPEC 209

RESULT 10
Q6IPUI_HUMAN
ID Q6IPUI_HUMAN PRELIMINARY; PRT; 313 AA.
AC Q6IPUI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Blood;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC071724; AAH71724.1; -; mRNA.
DR HSSP; P01850; 1KGC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR Hypothetical protein; Immunoglobulin domain.
KW SEQUENCE 313 AA; 34612 MW; BF890C926CE361BC CRC64;

Query Match 11.6%; Score 123.5; DB 2; Length 313;
Best Local Similarity 25.7%; Pred. No. 0.026;
Matches 46; Conservative 26; Mismatches 62; Indels 45; Gaps 8;

Qy 1 MAMMLLILIMVHPGSCALVWSQPPPE--IRTLEGSAPLPCSFNASQGRLAIGSVTWFRD 58
Db 6 LCWALLCLL---GAGSVETGVTQSPHLIKT-RGQVTLRCSSQSGH----NTVSWYQQ 56
Qy 59 EVVPG-----KEVRNGTPEFRGRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRV 110
Db 57 ALGQGFQFIFQYREEENG---RGNFPPRFSGLPQFPNYSSELNVNALELDDSAALYLCAS 112
Qy 111 EVLGLGVGT---GNGTRLVW-----EKEHPQLGAGTVLLLRAGFY 147
Db 113 SLGGPGLGETQYFGPGTRLLVLEDLKNVPFPEVAVPEPSAEISHTOKATLVCLATGFY 171

RESULT 11
Q6GMW3_HUMAN
ID Q6GMW3_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q6GMW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344854; AAK37537.1; -, mRNA.
 DR HSSP; P16410; 1A1.
 DR SMR; Q7JHJ0; 37-161.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008096; CTLA4.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003596; Ig v.
 DR PRINTS; PR01720; CTLANTIGEN4.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;
 Query Match 11.2%; Score 119; DB 2; Length 223;
 Best Local Similarity 26.7%; Pred. No. 0.044;
 Matches 54; Conservative 25; Mismatches 95; Indels 28; Gaps 6;
 QY 3 WMLLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVP 62
 DB 22 YTLFSLFLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPKATEVVRTVLRQADSQ 80
 QY 63 GKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL 113
 DB 81 VTEVCAATYMMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELM 134
 QY 114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFSLVAVGSTVYYQGKC 166
 DB 135 YPPPYMGINGTQIYVIDPEPCDPSDFLLWILAAVSSGLFFYSFLLTAVSLS-----KM 189
 QY 167 LTWKGRPRLPAPVAPLPPPC 188
 DB 190 LKRSPLTTGVVVKMPPTPEPC 211
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 AC Q7JHJ2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN CD152 protein precursor.
 GN Name=CTLA-4;
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinae; Cercocebus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344848; AAK37608.1; -, mRNA.
 DR HSSP; P16410; 1A1.

DR SMR; Q7JHJ2; 37-161.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008096; CTLA4.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003596; Ig v.
 DR PRINTS; PR01720; CTLANTIGEN4.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;
 Query Match 11.2%; Score 119; DB 2; Length 223;
 Best Local Similarity 26.7%; Pred. No. 0.044;
 Matches 54; Conservative 25; Mismatches 95; Indels 28; Gaps 6;
 QY 3 WMLLLILIMVHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVP 62
 DB 22 YTLFSLFLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPKATEVVRTVLRQADSQ 80
 QY 63 GKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL 113
 DB 81 VTEVCAATYMMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELM 134
 QY 114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFSLVAVGSTVYYQGKC 166
 DB 135 YPPPYMGINGTQIYVIDPEPCDPSDFLLWILAAVSSGLFFYSFLLTAVSLS-----KM 189
 QY 167 LTWKGRPRLPAPVAPLPPPC 188
 DB 190 LKRSPLTTGVVVKMPPTPEPC 211
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 ID Q9BDC4 MACMU PRELIMINARY; PRT; 223 AA.
 AC Q9BDC4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CD152 protein precursor.
 GN Name=CTLA-4;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344846; AAK37605.1; -, mRNA.
 DR HSSP; P16410; 1I85.
 DR SMR; Q9BDC4; 37-161.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008096; CTLA4.
 DR InterPro; IPR003599; Ig v.
 DR PRINTS; PR01720; CTLANTIGEN4.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;
 Query Match 11.2%; Score 119; DB 2; Length 223;
 Best Local Similarity 26.7%; Pred. No. 0.044;

Matches		54;	Conservative	25;	Mismatches	95;	Indels	28;	Gaps	6;
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Qy	63	GKEVRNGTPEFRGR	LAPLASSRFL	HD-----	HOAELHIRDVR	GH	DAS	IYVCR	VEVL	113
Db	81	VTEVCAATYMMGNELT-----	FLDDSI	CTGTSSGNQVNLTI	QGLRAMDTGL	I	CK	VELM	134	
Qy	114	---GLGVGTNGTRLVVEKEHPQLG	AGTVLL	RA-----	GFYAVSFLSV	AVG	STVY	YQ	KC	166
Db	135	YPPPYWGI	NGIQIYVIDPE	PCDSDFL	LWILA	AVSSGLFF	YSFLLT	AV	SL	189
Qy	167	LTKGPRRQLPA	VPA	PLPP	PC	188				
Db	190	LKKRSLTTGVYV	KMP	TEPEC	211					

Search completed: February 27, 2006, 18:03:03
Job time : 233 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 27, 2006, 18:03:18 ; Search time 47 Seconds
(without alignments)
353.570 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	11.1	223	2	US-08-228-208A-17
2	118.5	11.1	223	2	US-09-454-651B-17
3	118.5	11.1	232	2	US-09-949-016-11449
4	117	10.9	223	2	US-09-957-688C-1
5	116.5	10.9	223	2	US-09-949-016-6602
6	116.5	10.9	223	2	US-09-957-688C-2
7	116	10.9	226	2	US-09-311-784A-32
8	116	10.9	232	2	US-09-949-016-7589
9	116	10.9	232	2	US-09-949-016-7590
10	115	10.8	223	2	US-09-646-561-42
11	112	10.5	223	2	US-09-646-561-47
12	110	10.3	187	1	US-08-067-684-14
13	110	10.3	187	1	US-08-008-898-14
14	110	10.3	187	1	US-08-459-818-14
15	110	10.3	187	1	US-08-889-666-14
16	110	10.3	187	1	US-08-465-078-14
17	110	10.3	187	1	US-08-725-776-14
18	110	10.3	187	1	US-08-488-062-14
19	110	10.3	187	2	US-08-228-208A-14
20	110	10.3	187	2	US-08-253-783-36
21	110	10.3	187	2	US-08-454-651B-14
22	110	10.3	187	4	PCT-US95-06726-36
23	109	10.2	223	2	US-09-303-040-10
24	106.5	10.0	364	2	US-09-472-087-100
25	106	9.9	223	2	US-09-454-651B-18
26	106	9.9	270	2	US-09-082-593-10
27	105.5	9.9	236	2	US-09-049-672A-7

28	104.5	9.8	238	2	US-09-227-595-30	Sequence 30, Appl
29	104.5	9.8	238	2	US-09-227-595-32	Sequence 32, Appl
30	104.5	9.8	238	2	US-08-595-590B-30	Sequence 30, Appl
31	104.5	9.8	238	2	US-08-595-590B-32	Sequence 32, Appl
32	104	9.7	174	2	US-08-804-180C-4	Sequence 4, Appli
33	103.5	9.7	329	2	US-10-104-047-3709	Sequence 3709, Ap
34	103	9.7	267	1	US-08-416-336-2	Sequence 2, Appli
35	102.5	9.6	152	2	US-09-471-276-855	Sequence 855, App
36	102	9.6	223	2	US-08-228-208A-18	Sequence 18, Appl
37	102	9.6	239	2	US-09-828-995B-26	Sequence 26, Appl
38	102	9.6	377	2	US-09-227-595-24	Sequence 24, Appl
39	102	9.6	377	2	US-08-595-590B-24	Sequence 24, Appl
40	101.5	9.5	374	2	US-09-227-595-28	Sequence 26, Appl
41	101.5	9.5	374	2	US-09-227-595-28	Sequence 26, Appl
42	101.5	9.5	374	2	US-08-595-590B-26	Sequence 26, Appl
43	101.5	9.5	374	2	US-08-595-590B-28	Sequence 28, Appl
44	101	9.5	234	1	US-08-505-058-1	Sequence 1, Appli
45	101	9.5	234	1	US-08-459-818-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-228-208A-17
; Sequence 17, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-228-208A-17

Query Match 11.1%; Score 118.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.00037;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;
QY 6 LLILIMVHPCSC-ALMWSQPPEIRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGK 64
DB 24 LLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82
QY 65 EVRNGTPEFRGRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL-- 113
DB 83 EVCAATYMMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAAGSVTVYQKCLT 168
DB 137 PPVYLGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAVSL-----KMLK 191
QY 169 WKGPRQLPAVVPAPLPPPC 188
DB 192 KRSPLTTGVYVVKMPPEPEC 211

RESULT 2
US-09-454-651B-17
; Sequence 17, Application US/09454651B
; Patent No. 6887471
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; Ledbetter, Jeffrey A.
; Dams, Nitin K.
; Brady, William
; Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
; PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mandel & Adriano
; STREET: 35 N. Arroyo Parkway, Suite 60
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,651B
; FILING DATE: 06-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-Apr-1994
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.30USD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 626 395-7801
; TELEFAX: 626 395-0694
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-454-651B-17
Query Match 11.1%; Score 118.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.00037;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;
QY 6 LLILIMVHPCSC-ALMWSQPPEIRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGK 64
DB 24 LLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82
QY 65 EVRNGTPEFRGRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL-- 113
DB 83 EVCAATYMMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAAGSVTVYQKCLT 168
DB 137 PPVYLGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAVSL-----KMLK 191
QY 169 WKGPRQLPAVVPAPLPPPC 188
DB 192 KRSPLTTGVYVVKMPPEPEC 211

RESULT 3
US-09-949-016-11449
; Sequence 11449, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11449
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11449
Query Match 11.1%; Score 118.5; DB 2; Length 232;
Best Local Similarity 27.0%; Pred. No. 0.00039;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;
QY 6 LLILIMVHPCSC-ALMWSQPPEIRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGK 64
DB 33 LLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 91
QY 65 EVRNGTPEFRGRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL-- 113
DB 92 EVCAATYMMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELMYP 145
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAAGSVTVYQKCLT 168
DB 146 PPVYLGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAVSL-----KMLK 200
QY 169 WKGPRQLPAVVPAPLPPPC 188
DB 201 KRSPLTTGVYVVKMPPEPEC 220
RESULT 4
US-09-957-688C-1
; Sequence 1, Application US/09957688C

```
; Patent No. 6875904
; GENERAL INFORMATION:
; APPLICANT: LIU, YANG
; APPLICANT: ZHENG, PAN
; APPLICANT: LU, PING
; APPLICANT: MOSINGER, BEDRICH
; APPLICANT: MAY, KEN
; TITLE OF INVENTION: ANIMAL MODEL FOR IDENTIFYING AGENTS THAT INHIBIT OR ENHANCE
; FILE REFERENCE: CT1A4 SIGNALING
; CURRENT APPLICATION NUMBER: US/09/957,688C
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,089
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-957-688C-1

Query Match 11.0%; Score 117; DB 2; Length 223;
Best Local Similarity 26.1%; Pred. No. 0.00053;
Matches 52; Conservative 28; Mismatches 97; Indels 22; Gaps 7;

Qy 3 WMLLLILMVHPGSCALWVSQPPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFDRD--- 58
Db 22 FVALLTLFIPVFSEAIQVTPSVVLASSHGVSAPCEYSPSHNTDEV-RVTVLQRTNDQ 80
Qy 59 --EUVQKEVNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVL--- 113
Db 81 MTEVCATTFTKNTVGFLD--YPCSGTF-NESRVNLTIQGLRAVDTGLYCKVELMYPP 137
Qy 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL-----LLRAGFVAVSFLSVAGSVTVYQKCLTW 169
Db 138 PYFVGMGNGTQIYVIDPEPCDSDFLWLILVANSLGLFFYSFLVTAVSLS-----KMLKK 192
Qy 170 KGRPRQLPAVVPAPLPPPC 188
Db 193 RSPLTGGVYVVKMPTEPEC 211

RESULT 5
US-09-949-016-6602
; Sequence 6602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6602
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6602

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0006;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

Qy 6 LLILIMVHPGSC-ALWVSQPPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFDRVVPKG 64
Db 24 LLFFLLFIPVFCRAMHVAQPAVVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82
Qy 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL--- 113
Db 83 EVCAATYMTGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYP 136
Qy 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAGSVTVYQKCLT 168
Db 137 PYYVLGIGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLTAVSLS-----KMLK 191
Qy 169 WKGRPRQLPAVVPAPLPPPC 188
Db 192 KRSPLTTGGVYVVKMPTEPEC 211

RESULT 7
US-09-311-784A-32
; Sequence 32, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
```

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; Patent No. 6875904
; GENERAL INFORMATION:
; APPLICANT: LIU, YANG
; APPLICANT: ZHENG, PAN
; APPLICANT: LU, PING
; APPLICANT: MOSINGER, BEDRICH
; APPLICANT: MAY, KEN
; TITLE OF INVENTION: ANIMAL MODEL FOR IDENTIFYING AGENTS THAT INHIBIT OR ENHANCE
; FILE REFERENCE: CT1A4 SIGNALING
; CURRENT APPLICATION NUMBER: US/09/957,688C
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,089
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-688C-2

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0006;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

Qy 6 LLILIMVHPGSC-ALWVSQPPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFDRVVPKG 64
Db 24 LLFFLLFIPVFCRAMHVAQPAVVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82
Qy 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL--- 113
Db 83 EVCAATYMTGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYP 136
Qy 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAGSVTVYQKCLT 168
Db 137 PYYVLGIGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLTAVSLS-----KMLK 191
Qy 169 WKGRPRQLPAVVPAPLPPPC 188
Db 192 KRSPLTTGGVYVVKMPTEPEC 211

RESULT 6
US-09-957-688C-2
; Sequence 2, Application US/09957688C
; Patent No. 6875904
; GENERAL INFORMATION:
; APPLICANT: LIU, YANG
; APPLICANT: ZHENG, PAN
; APPLICANT: LU, PING
; APPLICANT: MOSINGER, BEDRICH
; APPLICANT: MAY, KEN
; TITLE OF INVENTION: ANIMAL MODEL FOR IDENTIFYING AGENTS THAT INHIBIT OR ENHANCE
; FILE REFERENCE: CT1A4 SIGNALING
; CURRENT APPLICATION NUMBER: US/09/957,688C
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,089
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-688C-2

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0006;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

Qy 6 LLILIMVHPGSC-ALWVSQPPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFDRVVPKG 64
Db 24 LLFFLLFIPVFCRAMHVAQPAVVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82
Qy 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL--- 113
Db 83 EVCAATYMTGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYP 136
Qy 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAGSVTVYQKCLT 168
Db 137 PYYVLGIGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLTAVSLS-----KMLK 191
Qy 169 WKGRPRQLPAVVPAPLPPPC 188
Db 192 KRSPLTTGGVYVVKMPTEPEC 211

RESULT 7
US-09-311-784A-32
; Sequence 32, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
```

APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human MB-1 Ig-alpha
US-09-311-784A-32

Query Match 10.9%; Score 116; DB 2; Length 226;
Best Local Similarity 27.3%; Pred. No. 0.00069;
Matches 50; Conservative 27; Mismatches 76; Indels 30; Gaps 9;
QY 4 MLLILIMVHPGSCALMVSO--PPPIRTLEGSSAFPLCSFNASQGRLAIGSVTWRDEVP 62
DB 18 LFLSAVYLGPGCOALMWHKVPASLMVSLGDEAHFQCPHNSNN-----ANVTWVR--VLH 71
QY 63 GKEVRNGT--PEPRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRVEVLGLGVGTG 120
DB 72 G-----NTWPPPEFLGP-----GEDPNGTLIIQNVKSHGGIYVCRVQEGNESYQOS 118
QY 121 NGTRLVVEKEHPQ----LGAGTV-LLLRAGFYAVSFLSVAGSTVYVYQKCLTWKGP 175
DB 119 CGTYLVRQPPPPRPFDMGEGTKNRIITAEIGIILLFCVVPGTLLLFKRK---WQNEKLG 175
QY 176 LPA 178
DB 176 LDA 178

RESULT 8
US-09-949-016-7589
Sequence 7589, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7589
LENGTH: 232
TYPE: PRT
ORGANISM: Human
US-09-949-016-7589

Query Match 10.9%; Score 116; DB 2; Length 232;
Best Local Similarity 27.3%; Pred. No. 0.00071;
Matches 50; Conservative 27; Mismatches 76; Indels 30; Gaps 9;
QY 4 MLLILIMVHPGSCALMVSO--PPPIRTLEGSSAFPLCSFNASQGRLAIGSVTWRDEVP 62
DB 24 LFLSAVYLGPGCOALMWHKVPASLMVSLGDEAHFQCPHNSNN-----ANVTWVR--VLH 77
QY 63 GKEVRNGT--PEPRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRVEVLGLGVGTG 120

DB 78 G-----NTWPPPEFLGP-----GEDPNGTLIIQNVKSHGGIYVCRVQEGNESYQOS 124
QY 121 NGTRLVVEKEHPQ----LGAGTV-LLLRAGFYAVSFLSVAGSTVYVYQKCLTWKGP 175
DB 125 CGTYLVRQPPPPRPFDMGEGTKNRIITAEIGIILLFCVVPGTLLLFKRK---WQNEKLG 181
QY 176 LPA 178
DB 182 LDA 184

RESULT 9

US-09-949-016-7590
Sequence 7590, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7590
LENGTH: 232
TYPE: PRT
ORGANISM: Human
US-09-949-016-7590

Query Match 10.9%; Score 116; DB 2; Length 232;
Best Local Similarity 27.3%; Pred. No. 0.00071;
Matches 50; Conservative 27; Mismatches 76; Indels 30; Gaps 9;
QY 4 MLLILIMVHPGSCALMVSO--PPPIRTLEGSSAFPLCSFNASQGRLAIGSVTWRDEVP 62
DB 24 LFLSAVYLGPGCOALMWHKVPASLMVSLGDEAHFQCPHNSNN-----ANVTWVR--VLH 77
QY 63 GKEVRNGT--PEPRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRVEVLGLGVGTG 120
DB 78 G-----NTWPPPEFLGP-----GEDPNGTLIIQNVKSHGGIYVCRVQEGNESYQOS 124
QY 121 NGTRLVVEKEHPQ----LGAGTV-LLLRAGFYAVSFLSVAGSTVYVYQKCLTWKGP 175
DB 125 CGTYLVRQPPPPRPFDMGEGTKNRIITAEIGIILLFCVVPGTLLLFKRK---WQNEKLG 181
QY 176 LPA 178
DB 182 LDA 184

RESULT 10

US-09-646-561-42
Sequence 42, Application US/09646561
Patent No. 6852847
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-1-C1-PCT
CURRENT APPLICATION NUMBER: US/09/646,561
CURRENT FILING DATE: 2000-09-19
PRIOR FILING DATE: 1998-03-19

Query Match	10.5%	Score 112;	DB 2;	Length 223;
Best Local Similarity	26.1%;	Pred. No. 0.0017;		
Matches 52;	Conservative 24;	Mismatches 95;	Indels 28;	Gaps 6;
Qy	6	LLILIMVHPGSCALWVSOPPEIRLTLEGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPCKE	65	
Db	25	LFSLLFPVTSKGMHVAQPAVVLAASSRCGVASFVCEYGSS-GNAAEVRVTVLROTGSMQTE	83	
Qy	66	VRNQTPEFRGRLAPLASSRFLHD-----HQAEHLHDRVGRGHDSAIYVCRVEVL----	113	
Db	84	VCAATYTVENELA-----FLDDSTGIGSSGNKVNLTIOGLRAMDGTGLYICKVELMYPP	137	
Qy	114	GLGVGTGNGTGLVVEKEHPQLGAGTIVLLRA---GFYAVGFLSVAVGSTVYVQGGKCLTW	169	
Db	138	PYVAGMNGTQYVIDPECPDPSDFLLILAAVSSGLFFYFGLITAVSLS-----XMLKK	192	
Qy	170	KGPRRQLPAVVPAPLPPPC	188	

RESULT 13
US-08-008-898-14
; Sequence 14, Application US/08008898
; Patent No. 5770197

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S
APPLICANT: Ledbetter, Jeffrey A
APPLICANT: Damle, Nitin K
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,898
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/723,617
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 7848
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-008-898-14

Query Match 10.3%; Score 110; DB 1; Length 187;
Best Local Similarity 26.7%; Pred. No. 0.0022;
Matches 50; Conservative 22; Mismatches 87; Indels 28; Gaps 6;
QY 18 ALMWSQPPEIRLTGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL 77
DB 1 AMHVAQPAVVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNEL 59
QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
DB 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLIRA-----GFYAVSFLSVAGSTVYVYQKCLTWKGRRLQPAVVP 181
DB 114 YVIDPEPCPSDFLLWILAAVSSGLFFYSFLLTAVSL-----KMLKRSPLTTGVYVKM 168
QY 182 APLPPPC 188
DB 169 PPTPEPC 175

RESULT 14
US-08-459-818-14
Sequence 14, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-14
Query Match 10.3%; Score 110; DB 1; Length 187;
Best Local Similarity 26.7%; Pred. No. 0.0022;
Matches 50; Conservative 22; Mismatches 87; Indels 28; Gaps 6;
QY 18 ALMWSQPPEIRLTGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL 77
DB 1 AMHVAQPAVVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNEL 59
QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
DB 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLIRA-----GFYAVSFLSVAGSTVYVYQKCLTWKGRRLQPAVVP 181
DB 114 YVIDPEPCPSDFLLWILAAVSSGLFFYSFLLTAVSL-----KMLKRSPLTTGVYVKM 168
QY 182 APLPPPC 188
DB 169 PPTPEPC 175
RESULT 15
US-08-889-666-14
Sequence 14, Application US/08889666
Patent No. 5885579
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

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OM protein - protein search, using sw model

Run on: February 27, 2006, 18:04:03 ; Search time 166 Seconds
(without alignments)
505.926 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MANWLLILIMVHFGSCALW.....APLPPCGSSAHLPPVPGG 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	1017.5	95.4	198	4	US-10-696-259-9
3	876	82.1	190	4	US-10-036-444-2
4	876	82.1	190	4	US-10-696-259-4
5	876	82.1	190	6	US-11-137-649-2
6	859	80.5	177	4	US-10-696-259-5
7	840.5	78.8	185	4	US-10-696-259-7
8	828.5	77.6	161	4	US-10-696-259-10
9	825	77.3	175	4	US-10-696-259-8
10	713	66.8	135	4	US-10-333-481-17
11	713	66.8	369	4	US-10-333-481-18
12	632	59.2	120	4	US-10-036-444-4
13	632	59.2	120	6	US-11-137-649-4
14	125.5	11.8	246	3	US-09-909-567B-49
15	125	11.7	212	3	US-09-898-195A-17
16	125	11.7	212	4	US-10-057-288-12
17	125	11.7	212	4	US-10-155-514-2
18	125	11.7	212	4	US-10-419-008-17
19	125	11.7	212	5	US-10-742-564A-6
20	125	11.7	212	5	US-10-740-645A-6
21	125	11.7	212	5	US-10-910-531-17
22	121.5	11.4	232	4	US-10-225-108A-12
23	121.5	11.4	232	4	US-10-461-148-6
24	118.5	11.1	139	4	US-10-312-495-6
25	118.5	11.1	223	5	US-10-741-600-894
26	118.5	11.1	223	5	US-10-461-000-17
27	117.5	11.0	223	4	US-10-383-201-20

28	117	11.0	223	6	US-11-052-559-1	Sequence 1, Appli
29	116.5	10.9	223	3	US-09-989-545-21	Sequence 21, Appl
30	116.5	10.9	223	3	US-09-928-267-18	Sequence 18, Appl
31	116.5	10.9	223	3	US-09-928-267-21	Sequence 21, Appl
32	116.5	10.9	223	4	US-10-225-519-8	Sequence 8, Appli
33	116.5	10.9	223	4	US-10-207-655-101	Sequence 101, App
34	116.5	10.9	223	5	US-10-688-845-24	Sequence 24, Appl
35	116.5	10.9	223	5	US-10-491-997-76	Sequence 76, Appl
36	116.5	10.9	223	6	US-11-052-559-2	Sequence 2, Appli
37	116.5	10.9	223	6	US-11-120-777-21	Sequence 21, Appl
38	116.5	10.9	382	4	US-10-207-655-316	Sequence 316, App
39	116.5	10.9	382	5	US-10-627-556-86	Sequence 86, Appl
40	116	10.9	226	4	US-10-038-107A-1	Sequence 1, Appli
41	116	10.9	226	4	US-10-371-525-32	Sequence 32, Appl
42	116	10.9	226	4	US-10-371-069-32	Sequence 32, Appl
43	116	10.9	226	4	US-10-371-645-32	Sequence 32, Appl
44	116	10.9	226	4	US-10-371-260-32	Sequence 32, Appl
45	116	10.9	226	4	US-10-411-010-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match 100.0%; Score 1067; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.7e-91;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MANWLLILIMVHFGSCALWVSPPEIRTLGSSAFILPCSFNASQGRLAIGSVTWFRDEV	60
Db	1	MANWLLILIMVHFGSCALWVSPPEIRTLGSSAFILPCSFNASQGRLAIGSVTWFRDEV	60
Qy	61	VPKVEVRNGTPEFRGLAPLASSRFLHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120
Db	61	VPKVEVRNGTPEFRGLAPLASSRFLHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120
Qy	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYVYQCKLTWKGPRLQPAVV	180
Db	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYVYQCKLTWKGPRLQPAVV	180
Qy	181	PAPLPPPCGSSAHLPPVPGG	201
Db	181	PAPLPPPCGSSAHLPPVPGG	201

RESULT 2
US-10-696-259-9

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; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-9

Query Match      95.4%; Score 1017.5; DB 4; Length 198;
Best Local Similarity 98.0%; Pred. No. 1.1e-86;
Matches 197; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 59
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
DB 60 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 118
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCLTWKGPRLPAVV 180
DB 119 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYHGKCLTWKGPRLPAVV 177
QY 181 PAPLPPPCGSAHLLPPVPGG 201
DB 178 PAPLPPPCGSAHLLPPVPGG 198

RESULT 3
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
; US-10-036-444-2

Query Match      82.1%; Score 876; DB 4; Length 190;
Best Local Similarity 89.2%; Pred. No. 1.7e-73;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCLTWKGPRLPAVV 172
DB 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHMGTHCHSSDGP 180
QY 173 RRLQPAVVPAVLPP 186
DB 181 R----GVPEPRCP 190

RESULT 5
US-11-137-649-2
; Sequence 2, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
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Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCLTWKGPRLPAVV 172
DB 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHMGTHCHSSDGP 180
QY 173 RRLQPAVVPAVLPP 186
DB 181 R----GVPEPRCP 190
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RESULT 4
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-4
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Query Match      82.1%; Score 876; DB 4; Length 190;
Best Local Similarity 89.2%; Pred. No. 1.7e-73;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASTYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCLTWKGPRLPAVV 172
DB 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHMGTHCHSSDGP 180
QY 173 RRLQPAVVPAVLPP 186
DB 181 R----GVPEPRCP 190
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RESULT 5
US-11-137-649-2
; Sequence 2, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
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Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 121 NGTRLVVEKEHPQLG 135
 Db 121 NGTRLVVEKEHPQLG 135

RESULT 12
 US-10-036-444-4
 ; Sequence 4, Application US/10036444
 ; Publication No. US20020142445A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INNATE PHARMA S.A.S.
 ; APPLICANT: UNIVERSITA DI GENOVA
 ; TITLE OF INVENTION: "NO. US2020142445A1el triggering receptor involved in natural
 ; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
 ; TITLE OF INVENTION: antibodies that identify the same"
 ; FILE REFERENCE: SEQ-FR-1060
 ; CURRENT APPLICATION NUMBER: US/10/036,444
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 09/440,514
 ; PRIOR FILING DATE: 1999-11-15
 ; PRIOR APPLICATION NUMBER: 09/456,199
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Human NK cell
 US-10-036-444-4

Query Match 59.2%; Score 632; DB 4; Length 120;
 Best Local Similarity 100.0%; Pred. No. 5.6e-51;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78
 Db 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

Qy 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138
 Db 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120

RESULT 13
 US-11-137-649-4
 ; Sequence 4, Application US/11137649
 ; Publication No. US20050221438A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INNATE PHARMA S.A.S.
 ; APPLICANT: UNIVERSITA DI GENOVA
 ; TITLE OF INVENTION: "Novel triggering receptor involved in natural
 ; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
 ; TITLE OF INVENTION: antibodies that identify the same"
 ; FILE REFERENCE: SEQ-FR-1060
 ; CURRENT APPLICATION NUMBER: US/11/137,649
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US/10/036,444
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 09/440,514
 ; PRIOR FILING DATE: 1999-11-15
 ; PRIOR APPLICATION NUMBER: 09/456,199
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Human NK cell
 US-11-137-649-4

Query Match 59.2%; Score 632; DB 6; Length 120;
 Best Local Similarity 100.0%; Pred. No. 5.6e-51;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78
 Db 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

Qy 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138
 Db 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120

RESULT 14
 US-09-909-567B-49
 ; Sequence 49, Application US/09909567B
 ; Publication No. US20030022257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Macina, Roberto A.
 ; APPLICANT: Nait, Manoj
 ; APPLICANT: Chen, Seiyu
 ; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
 ; FILE REFERENCE: DEX-0214
 ; CURRENT APPLICATION NUMBER: US/09/909,567B
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 60/219,834
 ; PRIOR FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 49
 ; LENGTH: 246
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-909-567B-49

Query Match 11.8%; Score 125.5; DB 3; Length 246;
 Best Local Similarity 27.1%; Pred. No. 0.0025;
 Matches 61; Conservative 20; Mismatches 73; Indels 71; Gaps 12;

Qy 1 MAMW-LLLILIMVHPGSCALWV-SQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRD 58
 Db 1 MAMW-PULLTLTLLTGLSGLQILTPPSASASLGASVTLTCSVSSDYKNL---EVDWQQ 57

Qy 59 EVVPGKEVR-----NGTPEFRGLAP-----LASSRFLHDHQAELHIRDVRGHDAS 104
 Db 58 R--PGKPRFVMRVGTGGVGVGRGADIPDRFVSVSGSLNRF-----LTIRNIEEDES 108

Qy 105 IYVCRVEVLGLGVGT-----GNGTRLV-----EKEHPQLGAGTVLLL 142
 Db 109 DYHCGTD---LGSHTSFVSVWFGGKTULTVLSQPKAAPSVTLPPSSEELQANKATLVCL 165

Qy 143 RAGFY--AVSFLSVAVGSTVYVGKCLTWKQPRRQLPAVVPAPLP 185
 Db 166 ISDFYPGAVT-----VAWKADSSPVKAGVETITTP 194

RESULT 15
 US-09-898-195A-17
 ; Sequence 17, Application US/09898195A
 ; Publication No. US20030083246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Robert
 ; APPLICANT: Carr, Suzanne
 ; APPLICANT: Hagerty, David
 ; APPLICANT: Peach, Robert J
 ; APPLICANT: Becker, Jean-Claude
 ; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
 ; TITLE OF INVENTION: CTLA4 MOLECULE
 ; FILE REFERENCE: D0030NP/30436.55USU1
 ; CURRENT APPLICATION NUMBER: US/09/898,195A
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: 60/215,913
 ; PRIOR FILING DATE: 2000-07-03
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 17
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-195A-17

Query Match      11.7%; Score 125; DB 3; Length 212;
Best Local Similarity 27.1%; Pred. No. 0.0023;
Matches 55; Conservative 26; Mismatches 92; Indels 30; Gaps 7;

Qy      4 MLLILIMVHP--GSCALWVSQPPEIRITLEGSSAFPCSFNASQGRLAIGSVTWFRDEVV 61
Db      10 LLSLVLALLPSPMASMAHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLQADS 68
Qy      62 PGKEVRNGTPEFRGR LAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEV 112
Db      69 QVTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVEL 122
Qy      113 L---GLGVGTGNGTRLVVEKEHPQLGAGTVLLLA-----GFYAVSELSVAVGSTVYYQ GK 165
Db      123 MYPPPYLIGNGTQIYVIDPEPCPSDFLLWILA AVSSGLFFYSFLLTAVSL S-----K 177
Qy      166 CLTWKPRRQLPAVVPAPLP PPC 188
Db      178 MLKKSPLTTGVVYKMPPTPEEC 200
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Search completed: February 27, 2006, 18:07:33
Job time : 167 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 18:04:53 ; Search time 19 Seconds
(without alignments)
157.491 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWMLLLILIMVHFGSCALW.....APLPFPCSSHLLPPVPGG 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
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3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	11.1	223	6	US-10-866-120-8
2	115	10.8	223	7	US-11-057-923-4
3	106.5	10.0	364	7	US-11-128-900-100
4	106	9.9	186	7	US-11-057-923-1
5	105	9.8	205	7	US-11-128-440-9
6	103.5	9.7	329	7	US-11-072-512-3709
7	102.5	9.6	252	7	US-11-054-515-1495
8	101.5	9.5	555	6	US-10-821-234-1015
9	98	9.2	240	7	US-11-000-463-248
10	98	9.2	508	7	US-11-072-512-3233
11	96.5	9.0	234	7	US-11-139-499-2
12	95	8.9	253	7	US-11-054-515-1545
13	94.5	8.9	236	7	US-11-000-463-815
14	94.5	8.9	247	7	US-11-062-186-62
15	94.5	8.9	247	7	US-11-033-039-877
16	94.5	8.9	252	7	US-11-062-186-66
17	94	8.8	708	6	US-10-511-538-229
18	93.5	8.8	203	7	US-11-062-186-70
19	93.5	8.8	206	7	US-11-062-186-69
20	93.5	8.8	208	7	US-11-062-186-63
21	93.5	8.8	213	7	US-11-062-186-67
22	93.5	8.8	224	7	US-11-062-186-64
23	93.5	8.8	229	7	US-11-062-186-68
24	92	8.6	215	6	US-10-374-954-7
25	92	8.6	241	5	US-09-978-360A-571

26	92	8.6	248	7	US-11-054-515-2070	Sequence 2070, Ap
27	91.5	8.6	232	7	US-11-000-463-755	Sequence 755, App
28	91	8.5	250	7	US-11-054-515-1484	Sequence 1484, Ap
29	90.5	8.5	628	7	US-11-080-991-108	Sequence 108, App
30	90	8.4	251	7	US-11-054-515-1207	Sequence 1207, Ap
31	89.5	8.4	110	6	US-10-982-440-50	Sequence 50, Appl
32	89.5	8.4	249	7	US-11-054-515-1570	Sequence 1570, Ap
33	89.5	8.4	250	7	US-11-054-515-1563	Sequence 1563, Ap
34	89.5	8.4	250	7	US-11-054-515-1564	Sequence 1564, Ap
35	89.5	8.4	250	7	US-11-054-515-1574	Sequence 1574, Ap
36	89.5	8.4	1700	6	US-10-453-372-398	Sequence 398, App
37	89.5	8.4	1700	6	US-10-453-372-412	Sequence 412, App
38	89.5	8.4	1700	6	US-10-453-372-414	Sequence 414, App
39	89.5	8.4	1700	6	US-10-453-372-416	Sequence 416, App
40	89.5	8.4	1700	6	US-10-453-372-418	Sequence 418, App
41	89	8.3	281	7	US-11-087-177-3	Sequence 3, Appli
42	89	8.3	282	6	US-10-055-877-127	Sequence 127, App
43	89	8.3	282	7	US-11-087-177-9	Sequence 9, Appli
44	89	8.3	304	7	US-11-087-177-4	Sequence 4, Appli
45	89	8.3	305	6	US-10-055-877-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-10-866-120-8
; Sequence 8, Application US/10866120
; Publication No. US2005027173A1
; GENERAL INFORMATION:
; APPLICANT: Chin, Li-Te
; TITLE OF INVENTION: METHOD FOR PRODUCING HUMAN ANTIBODIES OF AGONIST, ANTAGONIST, OF
; TITLE OF INVENTION: INVERSE AGONIST
; FILE REFERENCE: P7226/0600
; CURRENT APPLICATION NUMBER: US/10/866,120
; CURRENT FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(223)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P16410
; DATABASE ENTRY DATE: 2004-03-15
; RELEVANT RESIDUES: (1)..(223)
US-10-866-120-8

Query Match	11.1%;	Score 118.5;	DB 6;	Length 223;
Best Local Similarity	27.0%;	Pred. No. 0.00057;		
Matches	54;	Conservative	24;	Mismatches 93;
				Indels 29;
				Gaps 7;
Qy	6	LLILIMVHFGSC-ALWVSQPPEIRTELGSSAFPCSFNAGSLAIGSVTWFRDEWVPGK	64	
Db	24	LLFELLIPVECKAMHVAQPAVVLASSRGTAISFVCEY-ASPGKATEVTVTLROADSQVT	82	
Qy	65	EVRNGTPEFRGLRPLASSRFLHD-----HQAELHIRDVRGHDASIVCRVEVL--	113	
Db	83	EVCAATYMGNELT-----FLDDSICTGTSGNQVNLTIQGLRAMDTGLYICKVELMYP	136	
Qy	114	-GLGVGTGNGTRLVVEKEHPOLGAGTVLLRA----GEYAVSFILSVAGSVTVYQKCLT	168	
Db	137	PPYILGNGTQIYVIDPEPCPDSDFLLILAAVSSGLFFYSFLTAVSLS-----KMLK	191	
Qy	169	WKGPRRQLPAVVPAPLPPEC	188	
Db	192	KRSPLTTGVYVMPPEPEC	211	

```
RESULT 2
US-11-057-923-4
; Sequence 4, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; APPLICANT: Khare, Sanjay D.
; APPLICANT: Feige, Ulrich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
; TITLE OF INVENTION: IMMUNOGENIC THERAPEUTIC AGENT
; FILE REFERENCE: 54113.8008.WO00
; CURRENT APPLICATION NUMBER: US/11/057,923
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/35415
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 60/515,199
; PRIOR FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Murine CTLA-4
US-11-057-923-4

Query Match      10.8%; Score 115; DB 7; Length 223;
Best Local Similarity 26.1%; Pred. No. 0.0012;
Matches 52; Conservative 28; Mismatches 97; Indels 22; Gaps 7;

Qy 3 WMLLLILIMVHGSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRD----- 58
Db 22 FVALLTLFLIFVFESEAIOQTQPSVVVLASSHGVSFPCPSPSHTNDEV-RVTVLRTNDQ 80
Qy 59 --EVVPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVL--- 113
Db 81 MTEVCATTTKNTVGFLD--YPCSGTFF-NESRVNLTIOGLRAVDGTGLYCKVELMYPP 137
Qy 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL----LLRAGFYAVSFLSVAGSTVYVQKCLTW 169
Db 138 PYFVGMGNGTQIYVIDPEPCDFLLWILVAVSLGLFFYSLVSAVSL-----KMLKK 192
Qy 170 KGPRQLPAVVPAPLPPEC 188
Db 193 RSLPTTGVYVVKMPTEPEC 211

RESULT 3
US-11-128-900-100
; Sequence 100, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
```

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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-100

Query Match      10.0%; Score 106.5; DB 7; Length 364;
Best Local Similarity 28.0%; Pred. No. 0.013;
Matches 40; Conservative 20; Mismatches 62; Indels 21; Gaps 5;

Qy 4 MLLILIMVHP--GSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 61
Db 10 LLSLVALLFPMSAMAMHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADS 68
Qy 62 PGKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEV 112
Db 69 QVTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVEL 122
Qy 113 L---GLGVGTGNGTRLVVEKEHP 132
Db 123 MYPPPYLIGIGNGTQIYVIDPEP 145

RESULT 4
US-11-057-923-1
; Sequence 1, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; APPLICANT: Khare, Sanjay D.
; APPLICANT: Feige, Ulrich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
; TITLE OF INVENTION: IMMUNOGENIC THERAPEUTIC AGENT
; FILE REFERENCE: 54113.8008.WO00
; CURRENT APPLICATION NUMBER: US/11/057,923
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/35415
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 60/515,199
; PRIOR FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Full-length human CTLA-4 amino acid sequence
US-11-057-923-1

Query Match      9.9%; Score 106; DB 7; Length 186;
Best Local Similarity 26.6%; Pred. No. 0.0066;
Matches 49; Conservative 21; Mismatches 86; Indels 28; Gaps 6;

Qy 21 VSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPL 80
Db 3 VAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT-- 59
Qy 81 ASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRLVVE 128
Db 60 ----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYPPPYLIGIGNGTQIYVI 115
Qy 129 KEHPQLGAGTVLLRA-----GFYAVSFLSVAGSTVYVQKCLTWKGPRLQPAVVPAPL 184
Db 116 DPEPCPSDFLLWILAAVSSGLFFYSFLLTAVSL-----KMLKRSPLTTGVYVVKMPET 170
Qy 185 PPC 188
Db 171 EPEC 174
```

RESULT 5
US-11-128-440-9
; Sequence 9, Application US/11128440
; Publication No. US20050261478A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha
; APPLICANT: Brady, William A.
; APPLICANT: Grosmaitre, Laura S.
; APPLICANT: Law, Che-Leung
; APPLICANT: Dua, Raj
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; TITLE OF INVENTION: LYMPHOCYTE ACTIVATION
; FILE REFERENCE: 980034.408D1
; CURRENT APPLICATION NUMBER: US/11/128,440
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/646,381
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 09/252,150
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/108,683
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/075,274
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Llama llama
US-11-128-440-9

Query Match 9.8%; Score 105; DB 7; Length 205;
Best Local Similarity 24.9%; Pred. No. 0.0091;
Matches 50; Conservative 15; Mismatches 56; Indels 80; Gaps 12;
Qy 32 GSSAFPCSFNASQGR----LAIGSVTFWFRDEVPVGRKEVRNGTPEFRGRRLAPLASSRFLH 87
Db 15 GDSLRLSC--AASGRFTFTYAMG--WFRQ--APGKE----PEFVARISRVCSTFTYT 61
Qy 88 D-----HQAELHVRGHDASIIYCRVEVLGLVGTGNGTRLVVEKEHPQ 133
Db 62 DSVKGRFTISRDNKNTMYLQNMKAEDTAVYYCAAD-----SDYGPGR--SSEYDY 113
Qy 134 LGAGTVLLLRAGFVAVSFLSVAGSTVYYQKCLTWKGRQLPAVVPAPLP--C 188
Db 114 WQQT-----QTVSSE-----PKTPKPOPOPOPNPTTSKC 147
Qy 189 -----GSSAHLPPVP 199
Db 148 PKRPAPELLGSPSVFIPPKP 168

RESULT 6
US-11-072-512-3709
; Sequence 3709, Application US/11072512
; Publication No. US2006029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO

; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3709
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3709
Query Match 9.7%; Score 103.5; DB 7; Length 329;
Best Local Similarity 27.9%; Pred. No. 0.022;
Matches 29; Conservative 11; Mismatches 37; Indels 27; Gaps 3;
Qy 15 GSCALWVSQP-----PEIRTEGSAFLPCSFNASQGRLAIGSVTFWFRDEVPVGRKEVR 67
Db 159 GKTRLVVQVPVVIENGLPDLSTTEGSHAFPLCKARGSP-----PNTWTKD----- 205
Qy 68 NGTPEFRGLAPLASSRFLHQAELHVRGHDASIIYCRVE 111
Db 206 -----GQPVGAEGKFTIQSGELLVKNLEODAGTYTCTAE 242

RESULT 7
US-11-054-515-1495
; Sequence 1495, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1495
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1495
Query Match 9.6%; Score 102.5; DB 7; Length 252;
Best Local Similarity 29.0%; Pred. No. 0.02;

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Matches 36; Conservative 16; Mismatches 49; Indels 23; Gaps 6;
QY 15 GSCALWVSQPEIRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVVRGKEVR----- 67
Db 139 GSAQSVVTPPSVAAPGQRTVTS--GSSNIGINSVSWYQQ--LPGKAPKLLIYNNS 194
QY 68 --NGTPEPRGRRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGL-GVGTGNGT 123
Db 195 NRFSQVP---GRFSGSKSGT-----SASLAITGLQAEDEADYYCQSYDNSLNGVLFGGTT 246
QY 124 RLTV 127
Db 247 QLTV 250

RESULT 8
US-10-821-234-1015
; Sequence 1015, Application US/10821234
; Publication No. US2005025511441
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: DT_SEQ_genes Version 1.0
; SEQ ID NO 1015
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1015

Query Match 9.5%; Score 101.5; DB 6; Length 555;
Best Local Similarity 25.6%; Pred. No. 0.062;
Matches 40; Conservative 16; Mismatches 73; Indels 27; Gaps 5;
QY 2 AWMLLLILIMVHGPSALWVSQPEIRTE--GSSAFLPCSFNASQGRLAIGSVTWFRDEV 60
Db 59 AWMLLLLLASFTGRCPAGELETSDVTVTVLGDQAKLPCFYRGDSGE-QVGQVAWAVDA 117
QY 61 VPG-----KEVRNGTPEFRGLA-----PLASSRFLHDHQAELHIRDVRGHDAS 104
Db 118 GGAQELALLHSKYGLHVSAPYEGRVEQPPPPRNPDLGDSVLL-----RNAVQADEG 168
QY 105 IYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVL 140
Db 169 EYECRVSTFPAGSFQARLRRLVLPPLSLNPGPAL 204

RESULT 9
US-11-000-463-248
; Sequence 248, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
```

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; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 248
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-248

Query Match 9.2%; Score 98; DB 7; Length 240;
Best Local Similarity 25.0%; Pred. No. 0.049;
Matches 54; Conservative 26; Mismatches 76; Indels 60; Gaps 13;
QY 1 MAWMLLLILIMVHGPS---CALWVSQPEIRTELGSSAFLPCSFNASQGRLAIGSV--- 53
Db 6 MAWMLLLLLGLAY-GSGVDSETVVTQEPFSVSPGGTVTLTCGLNS-----GVSVDSE 57
QY 54 --TWFRDEVVVGKEVRNGTPEFRGL-APLASSRF---LHDHQAELHIRDVRGHDASIYV 107
Db 58 YPSWHQQ--TPGQPPR--TLIYNTHIRASGVSDRFGSGIVGNKAALTITGAQADDECVY 113
QY 108 CRVEVLGLGVGT-GNGTRLVV-----EKEHPQLGAGTVLLLRAGFY--AV 149
Db 114 C-VLYMGNDISLFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAV 172
QY 150 SFLSVAVGSTVYVYGGKCLTWKGRRLPAPVVPAPLP 185
Db 173 T-----VANKADSSPVKAGVETTP 192

RESULT 10
US-11-072-512-3233
; Sequence 3233, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
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; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3233
; LENGTH: 508
; TYPE: PRY
; ORGANISM: Homo sapiens
US-11-072-512-3233

Query Match          9.2%; Score 98; DB 7; Length 508;
Best Local Similarity 21.2%; Pred. No. 0.12; 78; Indels 130; Gaps 14;
Matches 63; Conservative 26; Mismatches 78; Indels 130; Gaps 14;

Qy 3 WMLLLILI-----MVHFG-----SCA-----LWVSOPPEIRILE 31
   |||: ||
   :||: ||
   :||: ||
Db 7 WLLLVAVLKGVQCEVQILESGGLVQPGGSLTILSRAAGSFIFSNYYTWVRQAQG-KGLE 65
   :||: ||
   :||: ||
   :||: ||
Qy 32 GSSAFPLCSFNASQGRLAIGSVTFWRDEVPVGEKVRNTPFPRGRRLAPLASSRFLHDHA 91
   |||: ||
   :||: ||
   :||: ||
Db 66 WVSS-----TAASGANTFYADSV-----KGR----FTVSRDENSENM 98
   :||: ||
   :||: ||
   :||: ||
Qy 92 ELHRDRVRGHDASTIYCRV--EVLGLGV-----GTGN-----GTRLVVEKEHP 132
   |||: ||
   :||: ||
   :||: ||
Db 99 YLOMSSLURGEDTIYCAKDGVNGLGVAMIVAGPCNVPRKWFDSWGQGTILVAVSSPSP 158
   :||: ||
   :||: ||
   :||: ||
Qy 133 QL-----CAGTVLLLRAGFYAVSFVLSV-----154
   :||: ||
   :||: ||
   :||: ||
Db 159 TSPKVPLSLCTQPDGNVVVIAQLVGQFPQEPFLSVTWSESGQVTARNPPSQDASGD 218
   :||: ||
   :||: ||
   :||: ||
Qy 155 -----AVGSTVYQCKLT-----WKGPRLQPAVVPAPLP PPPCGSSAHLLPVVP 199
   |||: ||
   :||: ||
   :||: ||
Db 219 YTTSSOLTLPATCLACKSVTCHVKHYTNPSQDVTVPCVPSTPTTPSPS--TPETP 273
   :||: ||
   :||: ||
   :||: ||

RESULT 11
US-11-139-499-2
; Sequence 2, Application US/11139499
; Publication No. US20050260205A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIEL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/11/139,499
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 234
; TYPE: PRY
; ORGANISM: Homo sapiens
US-11-139-499-2

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Best Local Similarity 22.5%; Pred. No. 0.065; 78; Indels 57; Gaps 8;
Matches 47; Conservative 27; Mismatches 78; Indels 57; Gaps 8;

Qy 5 LLLILLIVHFGS-CALWWSQPPEIRITLEGSSAFPLCSFNASQGRLAIGSVTFWRDE----- 59
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; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR FILING DATE: 2004-11-29
; PRIOR FILING DATE: 2002-11-08
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 815
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-815

Query Match      8.9%; Score 94.5; DB 7; Length 236;
Best Local Similarity 22.5%; Pred. No. 0.1;
Matches 48; Conservative 31; Mismatches 77; Indels 57; Gaps 10;

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Qy 59 EVVPEK-----EVRNGTPE-FRGR LAPLASSRFLHDHQAELHIRDVRGHDAIYV 107
Db 55 QLKPGQPLVVIHQDTKRPSGIPERFGSNS-----GNTATLTISGTQAMDEADYY 105
Qy 108 CRVEVLGLVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFYAVSFL 152
Db 106 CQAWDSSSYAFGGGTKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYP-GW 164
Qy 153 SVAVGSTVYVYQKCLTWKGRRLPAVVPAPLP 185
Db 165 TVA-----WKADSSPVKAGVETTP 184

RESULT 14
US-11-062-186-62
; Sequence 62, Application US/11062186
; Publication No. US20050272097A1
; GENERAL INFORMATION:
; APPLICANT: CALENOFF, EMANUEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; FILE REFERENCE: 21417-98470
; CURRENT APPLICATION NUMBER: US/11/062,186
; CURRENT FILING DATE: 2005-02-18
; PRIOR FILING DATE: 2004-02-18
; PRIOR FILING DATE: 2004-02-18

; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR FILING DATE: 2004-11-29
; PRIOR FILING DATE: 2002-11-08
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-08-03
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; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 815
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-815

; PRIOR APPLICATION NUMBER: 60/545,980
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 247
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; ORGANISM: Homo sapiens
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Best Local Similarity 27.3%; Pred. No. 0.11;
Matches 62; Conservative 26; Mismatches 84; Indels 55; Gaps 15;

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Qy 61 VPGKEV-----RNG-----TPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVC- 108
Db 72 -PFSRVVHLVRNGKDDQDQAPRYGRTELLKDA--IGEGKVTLRIRNVRFSDGGFTCF 128
Qy 109 -----RVEVLGLVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYV 162
Db 129 FRDHSYQEEA-----AMELKVEDPPFYWVSGVLVLL--AVLPVLLQLITVGLVFL- 176
Qy 163 QGKCLTWKGRRLPAVV-----PAPLPPPGCS-SAHLLPPVPG 200
Db 177 ---CLQYR-LRGKLRABEINLHRTFDPHFLRVCWKITLFIIVPVLG 219

RESULT 15
US-11-033-039-877
; Sequence 877, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RBH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR FILING DATE: 2005-01-11
; PRIOR FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
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; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-877

Query Match      8.9%; Score 94.5; DB 7; Length 247;
Best Local Similarity 27.3%; Pred. No. 0.11;
Matches 62; Conservative 26; Mismatches 84; Indels 55; Gaps 15;

Qy 5 LLLILLIMV---HPGSCALWVSPPEIRTLGSSAFPLPCSFNASQGRLAIG-SVTWFRDEV 60
Db 17 LLLLLLQVSSSYAGQFRVIGPRHP-IRALVGDVELPC--RISPGKNATGMEVGWYRP-- 71
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Qy 109 -----RVEVLGLVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYV 162
Db 129 FRDHSYQEEA-----AMELKVEDPPFYWVSGVLVLL--AVLPVLLQLITVGLVFL- 176
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Search completed: February 27, 2006, 18:07:57
Job time : 20 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search. **using frame_plus p2n model**

Run on: February 28, 2006, 06:25:45 ; Search time 3393 Seconds
(without alignments)
3367.384 Million cell updates/sec

Title: US-10-696-259-6
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Sequence: 1 MAMLLILILVHFGSCALW.....APLPPPCGSSAHLPPVPGG 201

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -HOST=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs803p
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1067	100.0	1061	6	CS032788 Sequence
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4	1067	100.0	1061	8	AF031137	AF031137 Homo sapi
5	1051	98.5	789	6	PTRS16006	AJ516006 Pan trogl
6	1039	97.4	834	6	BD087743	BD087743 BMOG, nov
7	1025	96.1	1116	6	CS032897	CS032897 Sequence
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14	876	82.1	606	6	AX148158	AX148158 Sequence
15	876	82.1	674	6	AX148147	AX148147 Sequence
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17	876	82.1	874	8	AF031138	AF031138 Homo sapi
c 18	872	81.7	15997	8	CR759886	CR759886 Human DNA
c 19	872	81.7	40160	8	EX248519	EX248519 Human DNA
c 20	872	81.7	55481	8	CR942185	CR942185 Human DNA
c 21	872	81.7	61358	8	AL929587	AL929587 Human DNA
c 22	872	81.7	81800	8	HSY14768	Y14768 Homo sapien
c 23	872	81.7	100409	8	EX927320	EX927320 Human DNA
c 24	872	81.7	101422	8	CR753892	CR753892 Human DNA
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c 26	872	81.7	132330	8	AL662801	AL662801 Human DNA
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c 29	872	81.7	349980	6	CS039420	CS039420 Sequence
c 30	859	80.5	496	6	CQ730908	CQ730908 Sequence
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c 33	840.5	78.8	110000	8	AB128049_00	AB128049 Macaca mu
c 34	840.5	78.8	182826	8	AC148688	AC148688 Macaca mu
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c 36	826	77.5	616	8	AY035215	AY035215 Macaca mu
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c 42	728	68.2	421	6	AX148156	AX148156 Sequence
c 43	713	66.8	405	6	AX367030	AX367030 Sequence
c 44	713	66.8	1110	6	AX367031	AX367031 Sequence
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ALIGNMENTS

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LOCUS	Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cdna clone MGC:59970 IMAGE:5934651), complete cds.				
DEFINITION	Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cdna clone MGC:59970 IMAGE:5934651), complete cds.				
ACCESSION	BC052582				
VERSION	BC052582.1 GI:30851220				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1024)				
	Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,				

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1024)
 Strausberg,R.
 Direct Submission
 Submitted (16-MAY-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgap@remail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Guinane,S., Guan,X., Gupta,J., Haghighi,P.,
 Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Lalic,P., Legaspi,R.,
 Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
 McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W.,
 Tsurgonov,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 47 Row: f Column: 19
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 24475831.

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 Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0
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 QY 41 PheAsnAlaSerGlnGlyValGluLeuAlaLeuGlySerValThrTriPheArgAspGluVal 60
 Db 329 TTCAATGCCAGCCCAAGGAGACTGGCCATTGGCTCCGTCACTGGTTCGAGATGAGGTG 388
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 Db 389 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGGCGCTTGGCCCTTT 448
 QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisLeuArgAspValArgGly 100
 Db 449 GCTTCTCCCGTTTCTCTCATGACCACCGAGCTGAGCTGCACATCCGGACGTCGGAGGC 508
 QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
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 Db 569 AATGGGACTCGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGGTGTGTACAGTCCTC 628
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 Db 629 CTCCTTCCGGCTGATCTATGCTGTACGCTTTCTCTGTGGCGTGGCGACACCGTC 688
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 Db 689 TATTACCGAGGCAATGCTCTGACCTGGAAGGTCCAAAGAGGAGCTGCCGGCTGTGGTC 748
 QY 181 ProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
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 QY 201 Gly 201
 Db 809 GGC 811
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 CS032788 1061 bp DNA linear PAT 10-MAR-2005
 LOCUS Sequence 2294 from Patent WO2005016962.
 DEFINITION CS032788
 ACCESSION CS032788
 VERSION CS032788.1 GI:60732157
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1
 REFERENCE
 AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
 TITLE Compositions and methods for the treatment of immune related
 diseases
 JOURNAL Patent: WO 2005016962-A 2294 24-FEB-2005;
 Genentech, Inc. (US)
 FEATURES
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 ORIGIN


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Hominidae; Homo.
1 (bases 1 to 1061)
Nalabolu,S.R., Shukla,H., Nallur,G., Farimoo,S. and Weissman,S.M.
Genes in a 220-kb region spanning the TNF cluster in human MHC
Genomics 31 (2), 215-222 (1996)
8824804
REFERENCE
2 (bases 1 to 1061)
Nalabolu,S.R., Raghunathan,A. and Weissman,S.M.
Analyses of the transcription pattern of B144 and 1C7, two immune
system related genes encoded near the TNF cluster
Unpublished (1997)
JOURNAL
3 (bases 1 to 1061)
Nalabolu,S.R., Raghunathan,A., Sivakanasundari,R. and Weissman,S.M.
Direct Submission
Submitted (23-OCT-1997) Genetics, Yale School of Medicine, 333
Cedar street, New Haven, CT 06510, USA
JOURNAL
FEATURES
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mat_peptide
448..867
misc_feature
695..750
/note="encodes putative membrane anchor site"
1003..1008
polyA_signal
ORIGIN
Alignment Scores:
Pred. No.: 8,1e-72 Length: 1061
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-696-259-6 (1-201) x AF031137 (1-1061)
QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCGTGGATGCTGTGCTCACTGATCATGGTCCATCCAGGATCTGCTCTCTGG 324
QY 21 ValSerGlnProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCAGCCCTCGAGATTCGTACCTCGTGAAGGATCTCTGCTCTCTGCGCTCC 384
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACCTGGTGTCCGAGATGAGGTG 444
QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCCAGGAGAGAGGTGAGGATGGAACCCAGAGATTTCAGGGGCGCTGCGCCACTT 504
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTTCGGTTTCTCCATGACCAACCGAGGTGAGCTGCATCCGGACGTGGAGGC 564

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QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyValGlyValGlyThrGly 120
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QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 ATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGGTACAGTCTCT 684
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValalaValGlySerThrVal 160
Db 685 CTCCTTCGGGCTGGATTTCTATCTGTACGCTTCTCTGTGGCCGTGGCAGCACCGTC 744
QY 161 TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLeuProAlaValVal 180
Db 745 TATTACACGGGCAATGTCTGACCTGGAAGGTCACAGAGGAGGAGTGGCGGCTGTGGTC 804
QY 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 805 CCAGCGCCCTCCACCACCATGTGGAGCTCAGACATCTGCTTCCCGCAGTCCCGGA 864
QY 201 Gly 201
Db 865 GGC 867
RESULT 5
PTRS16006 789 bp mRNA linear PRI 13-NOV-2003
LOCUS Pan troglodytes mRNA for Nkp30 (ncr3 gene).
DEFINITION AJ516006
ACCESSION AJ516006
VERSION AJ516006.1 GI:38322957
KEYWORDS ncr3 gene; Nkp30.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1
AUTHORS Blassoni,R.
TITLE Characterization of natural killer receptors in chimpanzees
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 789)
AUTHORS Blassoni,R.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2002) Blassoni R., Molecular Immunology, Istituto
Scientifico Tumori, Largo Rosanna Benzi 10, Genova 16132, ITALY
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52..657
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/evidence=experimental
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/translation="MAWMLLLILIMVHPGSCALMVSPPEIRTLGGSAFLPCSFNAS
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ORIGIN
Alignment Scores:
Pred. No.: 9,57e-71 Length: 789
Score: 1051.00 Matches: 199
Percent Similarity: 99.0% Conservative: 0
Best Local Similarity: 99.0% Mismatches: 2

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Query Match:	98.5%	Indels:	0
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Qy	21	ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer	40
Db	112	GTGTCCAGCCCTCGATTCGTACCTCGAAGGATCTCTGCTTCTCTGCTGCTCTCC	171
Qy	41	PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal	60
Db	172	TTCATATGCCAGCCCAAGGAGACTGGCCATTGGCTCCGTACGTGGTTCCGAGATGAGGTG	231
Qy	61	ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValArgLeuAlaProLeu	80
Db	232	GTTCACAGGAAGAGGTGAGGAATGAACCCCGAGTTTCAGGGGCCGCTGGCCCCACTT	291
Qy	81	AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly	100
Db	292	GCTTCTTCCCGTTTCTCCATGACCAACAGGCTGAGCTGCACATCCGGGACGTGCAGGC	351
Qy	101	HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly	120
Db	352	CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTCCGGACAGG	411
Qy	121	AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu	140
Db	412	AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCTCAGCTAGGGGCTGGTACAGTCTC	471
Qy	141	LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal	160
Db	472	CTCTTCGGGCTGGATTCTATGCTGTGCTCAGCTTCTCTCTGTGGCGTGGGACACCCGTC	531
Qy	161	TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVal	180
Db	532	TATTACCAAGGCAAAATGCTGACCTGGAAGGTCCAAAGAGCAGCTGCCGCGTGTGGTC	591
Qy	181	ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly	200
Db	592	CCAGCGCCCTCCCAACCACTATGGGAGCTCAGCACAGCTGCTTCCCCCAGTCCCAGGA	651
Qy	201	Gly 201	
Db	652	GGC 654	
BD087743 834 bp DNA linear PAT 27-AUG-2002			
LOCUS	BD087743		
DEFINITION	BMOG, novel member of myelin oligodendroglia glycoprotein family, and utilization thereof for immunomodulation.		
ACCESSION	BD087743		
VERSION	BD087743.1	GI:22633353	
KEYWORDS	JP 2001522589-A/3.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Browning, J.		
TITLE	BMOG, novel member of myelin oligodendroglia glycoprotein family, and utilization thereof for immunomodulation		
JOURNAL	Patent: JP 2001522589-A 3 20-NOV-2001;		
COMMENT	BIOGEN INC OS Homo sapiens (human) PN JP 2001522589-A/3 PD 20-NOV-2001 PF 06-NOV-1998 JP 2000519987 PR 07-NOV-1997 US 60/064761		

PI	JEFFREY BROWNING		
PC	C12N15/09,A61K48/00,A61P37/02,C07K14/47,C07K16/18,C07K19/00,		
PC	C12N1/15,		
PC	C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00 CC		
BMOG,	novel member of myelin oligodendroglia glycoprotein CC		
family,	and		
utilization	thereof for immunomodulation		
CC			
FH	Key		
FT	Location/Qualifiers		
FT	1..834		
FT	/organism='Homo sapiens (human)'		
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ORIGIN			
Alignment Scores:			
Pred. No.:	8.24e-70	Length:	834
Score:	1039.00	Matches:	200
Percent Similarity:	99.5%	Conservative:	0
Best Local Similarity:	99.5%	Mismatches:	1
Query Match:	97.4%	Indels:	1
DB:	6	Gaps:	0
US-10-696-259-6 (1-201) x BD087743 (1-834)			
Qy	1	MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp	20
Db	66	ATGGCTGGATGCTGTGCTCATCTTGATCATGTGCTCATCCAGGATCTGTGCTCTCTCGG	125
Qy	21	ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer	40
Db	126	GTGTCCAGCCCTCGATTCGTACCTCGAAGGATCTCTGCTTCTCTGCTGCTCTCTCC	185
Qy	41	PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal	60
Db	186	TTCATATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG	245
Qy	61	ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu	80
Db	246	GTTCACAGGAAGGAGGTGAGGAATGGAAACCCAGAGTTTCAG-GGGCGCTCGCCCCACTT	304
Qy	81	AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly	100
Db	305	GCTTCTTCCGTTTCTCTCCATGACCAACAGGCTGAGCTGCACATCCGGAGCTCGAGGC	364
Qy	101	HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly	120
Db	365	CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTCCGGACAGG	424
Qy	121	AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu	140
Db	425	AATGGGACTCGGCTGGTGGTGGAGAAAGAAACATCTCAGCTAGGGGCTGGTACAGTCTCT	484
Qy	141	LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal	160
Db	485	CTCCTTCGGGCTGGATTCTATGCTGTGTCAGCTTCTCTCTGTGGCGTGGGACGACCGTC	544
Qy	161	TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVal	180
Db	545	TATTACCAAGGCAAAATGCTGACCTGGAAAGGTCCAAAGAGGAGCTGCCGGCTGTGTC	604
Qy	181	ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly	200
Db	605	CCAGCGCCCTTCCCAACCACTATGGGAGCTCAGCACATCTGCTTCCCCCAGTCCCAGGA	664
Qy	201	Gly 201	
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RESULT 7			
CS032897			


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Db      745 TATTACAGGGCAATATGCAAAATCTACTCTCTCCGGATTCCCCCAACTCTGAACCTTC 804
Qy      167 -----LeuThrTrpLysGlyProArgGlnLeuProAlaValProAl 182
Db      805 CTTTCCACCAGGTCTGACCTGGAAAGGTCCAAGAAGGCAGCTGCCGCTGTGGTCCCAGC 864
Qy      182 aProLeuProProCysGlySerSerAlaHisLeuLeuProValProGlyGly 201
Db      865 GCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCCCAAGTCCAGGAGGC 922

RESULT 9
AF031136      1116 bp      mRNA      linear      PRI 18-NOV-1997
LOCUS      AF031136
DEFINITION      Homo sapiens lC7 precursor, mRNA, alternatively spliced, complete
c88.
ACCESSION      AF031136
VERSION      AF031136.1 GI:2623872
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1116)
Nalabolu,S.R., Shukla,H., Nallur,G., Parimoo,S. and Weisman,S.M.
Genes in a 220-Kb region spanning the TNF cluster in human MHC
Genomics 31 (2), 215-222 (1996)
8824804
REFERENCE
2 (bases 1 to 1116)
Nalabolu,S.R., Raghunathan,A. and Weisman,S.M.
Analyses of the transcription pattern of B144 and lC7, two immune
system related genes encoded near the TNF cluster
Unpublished (1997)
3 (bases 1 to 1116)
Nalabolu,S.R., Raghunathan,A., Sivakamasundari,R. and Weisman,S.M.
Direct Submission
Submitted (23-OCT-1997) Genetics, Yale School of Medicine, 333
Cedar street, New Haven, CT 06510, USA
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site not known; initiating methionine could also be one of
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/protein_id="AAB86578.1"
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448..795
mat_peptide
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/notes="encodes putative membrane anchor site"

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Alignment Scores:
Pred. No.: 1.3e-68 Length: 1116
Score: 1025.00 Matches: 200
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Best Local Similarity: 90.9% Mismatches: 1
Query Match: 96.1% Indels: 19
DB: 8 Gaps: 1

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Qy      1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
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Qy      21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db      325 GTGTCCCAAGCCCTTGAGATTCTGATTCGTGAAGGATCCTGTGCTTCTTCCCTGTCTCC 384
Qy      41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGlyVal 60
Db      385 TTCATGCCACGACCAAGGAGACTGGCCATTTGGCTTCCTCAGTGGTTCAGAGATGAGTG 444
Qy      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db      445 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCGCCTGGCCCACTT 504
Qy      81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleLeuArgAspValArgGly 100
Db      505 GCTTCTTCCCGTTTCTCTCCATGACCAACAGGCTGAGCTGCACATCCGGGACGTCCGAGGC 564
Qy      101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db      565 CATGACCCAGCATCTACGTGCCAGAGTGGAGTGTGGCCCTTGGTGTGGGACAGGG 624
Qy      121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db      625 AATGGGACTCGGCTGGTGGTGGAGAAAGACATCTCAGCTAGGGGCTGTGTACAGTCTCTC 684
Qy      141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db      685 CTCCTTCGGCTGGATTCTATGTCTCAGCTTCTCTCTGTGGCGGTGGGACAGCGTC 744
Qy      161 TyrTyrGlnGlyLys-Cys----- 165
Db      745 TATTACAGGGCAATATGCAAAATCTACTCTCTCCGGATTCCCCCAACTCTGAACCTTC 804
Qy      167 -----LeuThrTrpLysGlyProArgGlnLeuProAlaValProAl 182
Db      805 CTTTCCACCAGGTCTGACCTGGAAAGGTCCAAGAAGGCAGCTGCCGCTGTGGTCCCAGC 864
Qy      182 aProLeuProProCysGlySerSerAlaHisLeuLeuProValProGlyGly 201
Db      865 GCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCCCAAGTCCAGGAGGC 922

RESULT 10
BD087742      889 bp      DNA      linear      PAT 27-AUG-2002
LOCUS      BMOG, novel member of myelin oligodendroglia glycoprotein family,
DEFINITION      and utilization thereof for immunomodulation.
ACCESSION      BD087742
VERSION      BD087742.1 GI:22633352
KEYWORDS      JP 2001522589-A/2.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 889)
REFERENCE
AUTHORS      Browning,J.
TITLE      BMOG, novel member of myelin oligodendroglia glycoprotein family,
and utilization thereof for immunomodulation
JOURNAL      Patent: JP 2001522589-A 2 20-NOV-2001;
BIODEN INC
COMMENT      OS Homo sapiens (human)
PN JP 2001522589-A/2
PD 20-NOV-2001
PF 06-NOV-1998 JP 2000519987
PR 07-NOV-1997 US 60/064761
PI JEFFREY BROWNING
PC C12N15/09,A61K48/00,A61P37/02,C07K14/47,C07K16/18,C07K19/00,
C12N1/15,

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PC	C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12N15/00, C12N5/00 CC
BMOG	family, and novel member of myelin oligodendroglia glycoprotein CC
CC	utilization thereof for immunomodulation
FH	Key
FT	source
FT	1..889
FT	Location/Qualifiers
FEATURES	/organism="Homo sapiens (human)";
source	1..889
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Alignment Scores:	
Pred. No.:	1.34e-56 Length: 889
Score:	997.00 Matches: 199
Percent Similarity:	90.5% Conservative: 0
Best Local Similarity:	90.5% Mismatches: 2
Query Match:	93.4% Indels: 20
DB:	6 Gaps: 1
US-10-696-259-6 (1-201) x BD087742 (1-889)	
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Qy	21 ValSerGlnProProGluIleArgThrIleuGluGlySerSerAlaPheLeuProCysSer 40
Db	126 GTGTGCCAGCCCTCGAGATTCGTACCCCTGGAAAGGATCCTGTGCTTCTCTGCCCTGTCTCC 185
Qy	41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db	186 TTCATGCCAGCCCAAGGAGACTGGCCATTGGCTCCGTTCAGTGGTCCGAGATGAGGTG 245
Qy	61 ValProGlyLySgIuValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db	246 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCACAGATTTCAG-GGGCGCCTGGCCCCACTT 304
Qy	81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db	305 GCTTCTTCTCCGTCTTCTCCATGACCACCGAGCTGAGCTGCACATCCGGGACGTCCGAGGC 364
Qy	101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db	365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTCCGGACAGGG 424
Qy	121 AsnGlyThrArgLeuValValGluLySgIuHisProGlnLeuGlyAlaGlyThrValLeu 140
Db	425 AATGGGACTCGCTGGTGGTGGGAAAGAACATCCTCAGCTAGGGCTGGTACAGTCTCTC 484
Qy	141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db	485 CTCCTTCGGGCTGGATTCTATGCTGTCTCAGCTTTCTCTCTGTGGCCGTGGGACGACCGTC 544
Qy	161 TyrTyrGlnGlyLyS-Cys----- 165
Db	545 TATTACCAGGGCAATATGCAAAATCTACTCTCTCCGGATTCCCCCAACTCTGAACTTTC 604
Qy	167 -----LeuThrTrpLySgIyProArgArgGlnLeuProAlaValValProAl 182
Db	605 CCTTCCACCAAGTCTGACCTGGAAAGGTCCAAAGAGGACGTGCGGCTGTGGTCTCCAGC 664
Qy	182 aProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db	665 GCCCTCTCCACCAACCATGTGGAGCTCAGCACATCTGCTTCCCGCAGTCCCGAGGAGGC 722
RESULT 11	
BV174406/c	
LOCUS	BV174406 1613 bp DNA linear STS 10-JUN-2004
DEFINITION	sgnm71530 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.


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Db      933 CTCCTCTGGGCTGATCTATGCTGTGAGCTTTCTCTCTGTGGCGGTGGGAGACCGT 874
Qy      160 lTyTyTGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVa 180
Db      873 CTATTACCAGGCAAAATGCTGACCTGGAAGAGTCCAGAGAGNCAGCTACCGGCTGTGT 814
Qy      180 lProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGl 200
Db      813 CCCAGCGCCCTCCACCACCATGTGGAGCTCAGACATCTGCTTCCCCAGTCCCAGG 754
Qy      200 YGly 201
Db      753 AGGC 750

RESULT 12
LOCUS   AX148159                      573 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 13 from Patent WO0136630.
ACCESSION AX148159
VERSION   AX148159.1 GI:14347072
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS   Moretta,A., Bottino,C. and Blassoni,R.
TITLE      Novel triggering receptor involved in natural cytotoxicity mediated
          by human natural killer cells, and antibodies that identify the
          same
JOURNAL   Patent: WO 0136630-A 13 25-MAY-2001;
          Innate Pharma S.A.S. (FR) ; Universita di Genova (IT)
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source    1..573
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ORIGIN
Alignment Scores:
Pred. No.: 1.21e-57 Length: 573
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 6 Gaps: 2

US-10-696-259-6 (1-201) x AX148159 (1-573)

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Qy      21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db      61 GTGTCCAGCCCTCGAGATCGTACCTCGAAGGATCTCTGCTCTCTGCTGCTGCTCC 120
Qy      41 PheAlaAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db      121 TTCATGCCAGCAAGGAGAGACTGGCCATTCGCTCCGCTCAGCTGTTCCGAGATGAGGTG 180
Qy      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db      181 GTTCCAGGAGAGAGGTGAGGATGGAAACCCAGAGTTACAGGGCGGCTGGCCCACTT 240
Qy      81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db      241 GCCTTCTCCGCTTTCCTCCATGACCAACGAGCTGAGCTGACATCCGGGAGCTCGAGGC 300
Qy      101 HisAspAlaSerIleTyValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120

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Db      301 CATGACCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGTGTGGGACAGGG 360
Qy      121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db      361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCTCAGCTAGGGGCTGGTACAGTCTTC 420
Qy      141 LeuLeuArgAlaGlyPheTyAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db      421 CTCCTTCGGGCTGGAATCTATGCTGTCTCCTCTCTGTGGCGGTGGGAGCACCGCTC 480
Qy      161 TyTyTyGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db      481 TATTACCAGGCAAAATGCCACTGTGCATCGGGAACACACTGCCACTCTCAGATGGGCC 540
Qy      173 ArgArgGlnLeuProAlaValProAlaValProAlaProLeuProPro 186
Db      541 CGA-----GGGTGATTCCAGAGCCAGATGTCCTCC 570

RESULT 13
LOCUS   AB055881                      573 bp      mRNA      linear      PRI 01-DEC-2001
DEFINITION Homo sapiens NKp30 mRNA for natural killer cell receptor, complete cds.
ACCESSION AB055881
VERSION   AB055881.1 GI:17221621
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS   Sato,M., Yabe,T., Ohashi,J., Tsuchiya,N., Hanaoka,K., Tokunaga,K.
          and Juji,T.
TITLE      Identification of two novel single nucleotide polymorphisms in the
          NKp30 gene in human natural killer cells
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 573)
AUTHORS   Sato,M.
TITLE      Direct Submission
JOURNAL   Submitted (15-FEB-2001) Masako Sato, Japanese Red Cross Central
          Blood Center, Department of Research; Hiroo4-1-31, Shibuya-Ku,
          Tokyo 150-0012, Japan (E-mail:masako@cbc.jrc.or.jp,
          Tel:81-3-5485-6004, Fax:81-3-3406-7892)
FEATURES
source    1..573
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          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /chromosome="6"
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          /tissue_type="peripheral blood"
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          /product="natural killer cell receptor"
          /protein_id="BAB78472.1"
          /db_xref="GI:17221622"
          /translation="MAWMLLLILIMVHPSGSCALWVSQPPIRTLEGSAFLPCSFNAS
          QSLAIGSVTFWFRDEVPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHLDVRGHD
          ASLYVCRVEVLGVTGVTGCTRLVSKHPQLGAGTVLLLRAGFYAVSFLSVAVGSTV
          YGQKCHMGTHCHSSDGRGVIPEPRCF"
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          /genes="NKp30"
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          156
          /genes="NKp30"
          /replace="t"

ORIGIN
Alignment Scores:

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/organism="Homo sapiens"  
/mol_type="unassigned DNA"  
/db xref="taxon:9606"
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ORIGIN

Alignment Scores:					
Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	1-45e-57 876.00 90.2% 89.2% 82.1% 6	Length: Matches: Conservative: Mismatches: Indels: Gaps:	674 173 2 7 12 2		
<hr/>					
US-10-696-259-6 (1-201) x AX148147 (1-674)					
QY	1	MetAlaTrpMetLeuLeuLeulelleMerValHisProGlySerCysAlaLeuTrrp	20		
Dd	64	ATGGCCCTGGATCGTTGCATCTTGATCATGTGCCAGGATCCCTGTGTCCTCTG	123		
QY	21	ValSerGlnProProGlulleAargThrLeuGluGlySerSerAlaPheLeuProCysSer	40		
Dd	124	GtGTCCCACCCCCCTGAGATTGGTACCCTCGGAAGGATCCTGTGCTTCTGCCCTGCTCC	183		
QY	41	PheAsnAlaSerGlnGlyArgLeuAlalleGlySerValThrTrpPheArGaspGluVal	60		
Dd	184	TTCATATGCCAGCAAGGGAGACTGGCCATTGGCTCCGTACGTGTTCGAGATGAGGTG	243		
QY	61	ValProGlyLyseGluValArgAnsnClYThrProGluPheArGglyArgLeuAlaProLeu	80		
Dd	244	GTTCCAGGAAAGAAGGTGAGGAATGGAACCCACAGATTTCAGGGGGCCGCTGGGCCCACTT	303		
QY	81	AlaSerSerArgPheLeuHieAsphHisGlnAlaGluLeuHisIleArGaspValArGgLy	100		
Dd	304	GCITCTTCCGGTTTTCTTCNTGACCAACAGGCTGAGTGTCACATCCGGGACGTGCAGGC	363		
QY	101	HisAspAlaSerileTyRyValCysArgValGluVallLeuGlyLeuGlyValGlyThrGly	120		
Dd	364	CATGACCCAGCATCTACGTGTGCAGAGTGTGAGGTGTGGGCCCTTGGTGTGGGACAGGS	423		
QY	121	AnsglyThrArgLeuValvalGlysGluHiIsprodnLenGlyAlaGlyThrValLeu	140		
Dd	424	AANTGGACTTCGGCTGGTGGTAGAAAACAATCCTCAGCTAGGGGCTGGTACAGTCTCTC	483		
QY	141	LeuLeuArgAlaglyPhetyrAlaValSerPheLeuSerValAlaValGlySerrthrVal	160		
Dd	484	CTTCCTTCGGGCTGGATTTCTATGCTGTACGCTTTCTCTGTGGCCGTGGGACACCGTC	543		
QY	161	TyrTyrgInGLys-----CylLeuthrTrpLysGlyPro	172		
Dd	544	TATTACAGGGCAAATGCCACTGTCCATGGGAACACATGCCACTCCTCAGATGGGCC	603		
QY	173	ArgArgGlnLeuProAlavalProAlaProLeuProPro	186		
Dd	604	CGA-----GSGRTGTATCCAGAGCCAGATGTGCC	633		

Search completed: February 28, 2006, 10:53:02
Job time : 3400 secs

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Result No.	Query	Score	*			ID	Description
			Match	Length	DB		
1	ADVA3954	1067	100.0	606	14	ADVA3954	Human psy
2	AEA40217	1067	100.0	606	14	AEA40217	Human nat
3	ADXD01458	1067	100.0	1061	14	ADXD01458	Human tol
4	ADV16488	1067	100.0	1061	14	ADV16488	DNA encod

DR WPI; 2005-031682/03.

XX New microarray comprising probes for genes involved in

PT psychoneuroendocrine (PNI) activity, useful in diagnosing a

PT condition associated with PNI activity, e.g., inflammatory or infectious

PT diseases.

XX Claim 1; SEQ ID NO 1582; 254pp; English.

XX The invention relates to a new microarray which comprises probes for

CC genes involved in psychoneuroendocrine (PNI) activity. The

CC microarray is useful in diagnosing a condition associated with PNI

CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,

CC cancer and infection. The present sequence represents a

CC psychoneuroendocrine gene expressed sequence tag. Note the

CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to

CC SEQ ID NO 1829 are provided.

XX

SQ Sequence 606 BP; 105 A; 182 C; 184 G; 135 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.26e-85 Length: 606

Score: 1067.00 Matches: 201

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 14 Gaps: 0

US-10-696-259-6 (1-201) x ADV43954 (1-606)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20

Db 1 ATGGCTGGAGTCTGCTGCTATCTTATCATGTCATCCAGATCTGCTGCTCTGG 60

QY 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40

Db 61 GTGTCCCAAGCCCTGAGATTCGTACCTGACCTGGAAGATCTCTGCTTCTGCTGCTGCC 120

QY 41 PheAlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuVal 60

Db 121 TTCAATGCCACCAAG 180

QY 61 ValProGlyValGluValArgAsnGlyThrProGluPheArgGlyValGluAlaProLeu 80

Db 181 GTTCAGGAG 240

QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100

Db 241 GCTTCTTCCGCTTCTCTCCATGACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 101 HisAlaSerIleThrValCysArgValGluValLeuGlyValGlyThrGly 120

Db 301 CATGACGCGCATCATCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

QY 121 AsnGlyThrArgLeuValValGluValGluHisProGlnLeuGlyValGlyThrValLeu 140

Db 361 AATGGAGATCGGCTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 141 LeuLeuArgAlaGlyPheTyraValSerPheLeuSerValAlaValGlySerThrVal 160

Db 421 CTCCTTCGGCTGGATTCATCTGTCAGCTTCTCTCTGTGGCCGTCGGGACAGCCGTC 480

QY 161 TyrTyrGlnGlyValCysLeuThrTrpValGlyProArgGlnLeuProAlaValVal 180

Db 481 TATTACCAAGGGAATATGTCACCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly 200

Db 541 CCAGCGCCCTCCACCAACCATGTCGGAGCTCAGACATCTCTCTCTCTCTCTCTCTCTCT 600

QY 201 Gly 201

Db 601 GGC 603

RESULT 2

AEA40217

ID AEA40217 standard; DNA; 606 BP.

XX

AC AEA40217;

XX

DT 11-AUG-2005 (first entry)

XX

DE Human natural cytotoxicity receptor associated DNA, SEQ ID NO:23.

XX

KW natural cytotoxicity receptor; natural killer cell; lymphocyte; membrane;

KW tumor; cell disintegration; antibody; hyperproliferation; cytostatic; ds.

XX

OS Homo sapiens.

XX

PN WO2005051973-A2.

XX

PD 09-JUN-2005.

XX

PF 24-NOV-2004; 2004WO-IL001081.

XX

PR 25-NOV-2003; 2003US-0524648P.

XX

PA (YISS) YISSUM RES & DEV CO.

PA (UYNE) UNIV BEN-GURION NEGEV RES & DEV.

XX

PI Mandelboim O, Porgador A;

XX

WP; 2005-405348/41.

XX

New peptides derived from specific natural cytotoxicity receptors and

capable of binding to membrane-associated biomolecules of tumor cells,

useful for targeting tumor cells to diagnose or treat benign and/or

malignant tumors.

Disclosure; SEQ ID NO 23; 86pp; English.

The invention relates to isolated peptide fragments of a natural

cytotoxicity receptor (NCR) of natural killer (NK) cells, or active

fragments, analogs or derivatives, wherein the peptide fragment is

capable of binding to a membrane-associated biomolecule of a tumor cell,

and the biomolecule comprises at least one sulfated polysaccharide, and

serves as the binding site of the NCR mediating the lysis of tumor cells

by NK cells, with the proviso that the peptide is other than a full

length NCR polypeptide or an isolated NCR extracellular domain. Also

described are: (1) an antibody that recognizes an epitope on a target

membrane-associated biomolecule of a tumor cell, the biomolecule

comprising at least one sulfated polysaccharide and mediating the lysis

of tumor cells by NK cells via the NCR; (2) a method of targeting a tumor

cell in a subject via an NCR-dependent mechanism; and (3) a method of

identifying peptides derived from NCR which are capable of binding to a

membrane-associated sulfated polysaccharide of a tumor cell. The peptide

fragment comprises 7-120, 8-100 or less than about 50 contiguous amino

acids. The peptide is a fragment of NCR selected from Nkp44, Nkp30 and

Nkp46. It is a fragment of the D2 domain of Nkp46 comprising a sequence

fully defined in the specification (SEQ ID NOS: 1 and 2), or a fragment

of Nkp30 selected from a sequence fully defined in the specification (SEQ

ID NOS: 3 and 4). Alternatively, the peptide is a fragment of Nkp44

having a sequence fully defined in the specification (SEQ ID NO: 5). The

membrane-associated biomolecule is selected from a glycosaminoglycan and

a proteoglycan. The antibody is capable of blocking the binding of NK

cells via NCR to membrane-associated sulfated polysaccharide biomolecules

in a cell, therefore, inhibiting NCR-dependent cell lysis associated with

autoimmunity. The peptides and antibodies of the invention are useful for

targeting a tumor cell in a subject via an NCR-dependent mechanism. The

composition and methods of the invention are useful for targeting tumor

cells to diagnose and/or treat benign and malignant tumors or

proliferative diseases. This sequence represents DNA of unknown function

relating to the present invention. Note: This sequence given as SEQ ID

No:23 in the Sequence Listing is not mentioned elsewhere in the

specification.

SQ Sequence 606 BP; 105 A; 182 C; 184 G; 135 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,26e-85 Length: 606
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-696-259-6 (1-201) x AEA40217 (1-606)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCTGGATGCTGTCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCGG 60
QY 21 ValSerGlnProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCCCTGAGATTGCTACCTTGAAGGATCCTCTGCCCTTCTGCCCTGCTCC 120
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCACCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG 180
QY 61 ValProGlyLysGluValAlaArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCAGGGAAGGAGGTGAGGAATGGAACCCACAGATTTCAGGGCCGCTGGCCCACTT 240
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCCTTCTCCCTTTCCTCCATGACACACAGGCTGAGCTGCACATCCGGGAGCTGCGAGGC 300
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGAGCCAGCATCTAGCTGTGAGAGTGAGGTGCTGGGCCCTTGGTTCGGACAGGG 360
QY 121 AsnGlyThrArgLeuValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGAGCTCGGCTGGTGGTGGAGAAAGACATCTCAGCTAGGGCTGGTACAGTCTCTC 420
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGAATTCTATGCTGTACGCTTCTCTGTGGCGCTGGGACAGCCGTC 480
QY 161 TyrTyrGlnGlyLysCysLeuThrTriPlysglyProArgGlnLeuProAlaValVal 180
Db 481 TATTACAGGGCAATGTCTGACCTGGAAGGTCCAAGAGCGAGCTGCCGGCTGTGTC 540
QY 181 ProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProValProGly 200
Db 541 CCAGGCCCCCTCCACACCATGTGGGAGCTCAGACATCTGCTTCCCCCAGTCCAGGA 600
QY 201 Gly 201
Db 601 GGC 603

RESULT 3

ADX01458
ID ADX01458 standard; DNA; 1061 BP.

AC ADX01458;

DT 21-APR-2005 (first entry)

XX Human tolerance target molecule #31.

DE Screening; immune disorder; autoimmune disease; transplant rejection;
KW diabetes mellitus; arthritis; rheumatoid arthritis; multiple sclerosis;
KW myasthenia gravis; systemic lupus erythematosus; Hashimoto's disease;
KW dermatitis; psoriasis; ulcerative colitis; scleroderma;
KW female genital tract inflammation; Crohn's disease; sarcoidosis;
KW pulmonary fibrosis; immunosuppressive; antidiabetic; antiarthritic;
KW antirheumatic; neuroprotective; muscular-gen.; antiinflammatory;

KW dermatological; antithyroid; antipsoriatic; antiulcer;
KW gastrointestinal-gen.; respiratory-gen.; cytostatic; virucide; gene; ds.

OS Homo sapiens.

XX WO2005010215-A2.

XX 03-FEB-2005.

XX 19-JUL-2004; 2004WO-US023309.

XX 17-JUL-2003; 2003US-0488502P.

XX (TOLE-) TOLERRX INC.

PI Rao P, Snyder J, Bagley A;

XX WPI; 2005-123168/13.

XX Identifying a tolerance modulatory compound, useful for reducing T
effector (Teff) cell function or increasing T regulatory (Treg) cell
function, by assaying for expression or activity of Treg marker and Teff
marker.

XX Disclosure; SEQ ID NO 31; 149pp; English.

XX The invention relates to a method of identifying a tolerance modulatory
compound comprising assaying for expression or activity of at least one T
regulatory (Treg) marker and at least one T effector (Teff) marker, where
a change in expression or activity of the Treg marker or the Teff marker
and/or an inverse change in expression or activity of the Teff marker
identifies the test compound as a tolerance modulatory compound. The
method comprises contacting a T cell with a stimulating agent and a test
compound and assaying for expression or activity of at least one Treg
marker and at least one Teff marker. The invention also relates to a
method of identifying a tolerance promoting compound and a method of
identifying a tolerance suppressing compound. The method is useful for
identifying a tolerance modulatory compound, e.g. a tolerance promoting
compound or a tolerance suppressing compound. The methods are useful for
reducing T effector cell function or for increasing T regulatory cell
function. The modulator identified can be used in an animal model to
determine the efficacy, toxicity or side effects of treatment with the
modulator. Tolerance modulatory compounds are also useful for treating
immune-mediated diseases, e.g. autoimmune diseases, transplant rejection
or unwanted immune responses to chronically administered therapeutic
proteins. Diseases include diabetes mellitus, arthritis, rheumatoid
arthritis, multiple sclerosis, myasthenia gravis, systemic lupus
erythematosus, Hashimoto's disease, dermatitis, psoriasis, ulcerative
colitis, scleroderma, female genital tract inflammation, Crohn's disease,
sarcoidosis and pulmonary fibrosis. The compounds are further useful for
enhancing immune responses, e.g. to tumors or viruses to which the body
may have become tolerant. This sequence represents a human tolerance
target molecule of the invention.

XX SQ Sequence 1061 BP; 212 A; 320 C; 288 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.46e-85 Length: 1061
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-696-259-6 (1-201) x ADX01458 (1-1061)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCTGGAGTGTGTGCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCGG 324
QY 21 ValSerGlnProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCAGCCCCCTGAGATTGCTACCTTGAAGGATCCTCTGCCCTTCTGCCCTGCTCC 384

DE Human B-cell myelin oligodendrocyte glycoprotein BMOG cDNA.

KW MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
 KW signal transduction; immunomodulator; antiinflammatory;
 KW autoimmune disease; inflammation; gene therapy; diagnosis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 66..670
 FT CDS

FT /tag= a

FT /transl_except= (pos:291..292, aa:Arg)

FT /note= "this codon contains an apparent 1 nucleotide
 deletion, which alters the reading frame"

FT sig_peptide 66..101

FT /tag= b

FT mat_peptide 102..667

FT /tag= c

XX WO9923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

XX P-PSDB; AAY06403.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 1; Page 42; 43pp; English.

XX This DNA sequence encodes human BMOG, a novel member of the B cell myelin
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
 CC identified. The protein is present primarily in the spleen, in lymph
 CC nodes and in germinal centre B cells. It may have immunoregulatory
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
 CC producing BMOG using these transformed host cells are also provided. BMOG
 CC polypeptides can be used for modulating the immune system of a subject or
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it
 CC with a soluble BMOG protein. The nucleic acid can be used for gene
 CC therapy. The protein can also be used to target a toxin, imaging agent or
 CC radionuclide to a cell expressing BMOG. (All claimed)

SQ Sequence 834 BP; 152 A; 258 C; 232 G; 192 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.01e-82 Length: 834
 Score: 1039.00 Matches: 200
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 1
 Query Match: 97.4% Indels: 1
 DB: 2 Gaps: 0

US-10-696-259-6 (1-201) x AAX59349 (1-834)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20

Db 66 ATGGCTGGATGCTGTTCTCATCTGATCATGTGTCATCCAGGATCTGTGCTCTCG 125

Qy 21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40

Db 126 GTGTCCAGGCCCTTGAGATGTCGTACCTGGAAGATCCTCTGCTTCCCTCCCTGCTCC 185

Qy 41 PheAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 Db 186 TTCAATGCCAGCAAGGAGAGACTGGCCATTGGCTCCGTCAGCTGGTCCGAGATGAGGTG 245

Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
 Db 246 GTTCCAGGGAAGGAGGTGAGGAATGGAAACCCAGAGTTTCAG-GGGCGGCTGGCCCACTT 304

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 305 GCTTCTTCCCGTTTCTCCATGATGACCAACAGGCTGAGCTGCACATCCGGAGCTGGAGGC 364

Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
 Db 365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGGTGGCCCTTGGTGTGGGACAGGG 424

Qy 121 AsnGlyThrArgLeuValValGluValGluHisProGlnLeuGlyAlaGlyThrValLeu 140
 Db 425 AATGGACTCGGCTGGTGGTGGAGAAAGAAATCTCTAGCTAGGGGCTGGTACAGTCTCTC 484

Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 Db 485 CTCCTCGGCTGGATTCTATGCTGTGAGCTTCTCTCTGTCGGCGTGGGAGCAGCCCTC 544

Qy 161 TyrTyrGlnGlyLysCysLeuThrThrTrpLysGlyProArgArgGlnLeuProAlaValVal 180
 Db 545 TATTACCAGGGCAAAATGCTGACCTGGAAAGGTCCAAGAGGACAGCTGCCGGCTGTGTC 604

Qy 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuLeuProProValProGly 200
 Db 605 CCAGCGCCCTCCACCACCATGTGGAGAGTCCAGCACATCTGCTTCCCCCAGTCCCAGGA 664

Qy 201 Gly 201

Db 665 GGC 667

RESULT 6

ADY16597

ID ADY16597 standard; DNA; 1116 BP.

AC ADY16597;

XX 05-MAY-2005 (first entry)

DT DNA encoding a PRO polypeptide, SEQ ID NO 2403.

DE Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; de; gene; diagnosis.

XX Homo sapiens.

OS WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
 XX Claim 1; SEQ ID NO 2403; 158pp; English.

```
XX CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX SQ Sequence 1116 BP; 224 A; 343 C; 293 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,49e-81 Length: 1116
Score: 1025.00 Matches: 200
Percent Similarity: 90.9% Conservative: 0
Best Local Similarity: 90.9% Mismatches: 1
Query Match: 96.1% Indels: 19
DB: 14 Gaps: 1

US-10-696-259-6 (1-201) x ADY16597 (1-1116)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCCTGGATGCTGTGCTCATCTTGCATCATGCTCCATCCAGGATCCTGTGCTCTCTGG 324
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCACGCCCCCTGAGATTGCTGACCTGGAAGATCTCTGCTTCTGCTGCTGCTGCC 384
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCAATCGACCGCAAGGAGAGCTGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG 444
Qy 61 ValProGlyGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCAGGAAAGGAGGTGAGAAATGGAACCCAGAGTTTCAGGGGCGGCTCGCCCCACTT 504
Qy 81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTTCCCTTCTCTCCATGACCCAGAGCTGAGCTGCACTCCGGAGCTGGAGGC 564
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 565 CATGAGCCAGCATCTACGTGTGCAGAGTGCAGAGTGTGGGCTTGGTGTGGGACAGGG 624
Qy 121 AsnGlyThrArgLeuValValGluGlyHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 AATGGACTCGCTGTGTGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTCTCT 684
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 695 CTCCTTCGGGCTGGATTCTATGCTGTACGCTTCTCTGTGGCGGCGGAGCACCGCTC 744
Qy 161 TyrTyrGlnGlyLys-Cys----- 166
Db 745 TATTACAGGCAATATATGCCAAATCTACTCTCCGGATTCCCCCAACTCTGAATTTTC 804
Qy 167 -----LeuThrTrpLysGlyProArgArgGlnLeuProAlaValProAl 182
Db 805 CTTTCCACAGGCTCTGACCTGGAAGGTCCAGAAAGGAGCGCTGCCGGTGTGGTCCAGC 864
Qy 182 aProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 865 GCCCTTCCACACCATGTGGAGGCTCAGCATCTGCTTCTTCCCGAGTCCCGAGGAGGC 922

RESULT 7
ID AAX59348
XX AAX59348 standard; cDNA; 889 BP.
AC AAX59348;
XX
XX 20-SEP-1999 (first entry)
XX
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG cDNA.
DE
```

```
XX BMOG: B-cell myelin oligodendrocyte glycoprotein; human;
KW signal transduction; immunomodulator; antiinflammatory;
KW autoimmune disease; inflammation; gene therapy; diagnosis; ss.
XX Homo sapiens.
FH Location/Qualifiers
FT 66..598 a
FT /*tag=
FT /transl_except= (pos:291..292, aa:Arg)
FT /notes="this codon contains an apparent 1 nucleotide
FT deletion, which alters the reading frame"
FT sig_peptide 66..101
FT /*tag= b
FT mat_peptide 102..595
FT /*tag= c
XX
XX WO9923867-A2.
XX
XX 20-MAY-1999.
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX P-PSDB; AAY06402.
XX
XX Novel B-cell myelin oligodendrocyte glycoproteins.
XX
XX Claim 1; Page 41; 43pp; English.
XX
XX This DNA sequence encodes human BMOG, a novel member of the B cell myelin
XX oligodendrocyte glycoprotein family that is expressed by germinal centre
XX B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
XX identified. The protein is present primarily in the spleen, in lymph
XX nodes and in germinal centre B cells. It may have immunoregulatory
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to
XX regulate the immune system in autoimmune or inflammatory disease. Vectors
XX comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
XX producing BMOG using these transformed host cells are also provided. BMOG
XX polypeptides can be used for modulating the immune system of a subject or
XX to inhibit signal transduction in a cell expressing BMOG by contacting it
XX with a soluble BMOG protein. The nucleic acid can be used for gene
XX therapy. The protein can also be used to target a toxin, imaging agent or
XX radionuclide to a cell expressing BMOG. (All claimed)
XX
XX Sequence 889 BP; 164 A; 281 C; 237 G; 207 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,72e-79 Length: 889
Score: 997.00 Matches: 199
Percent Similarity: 90.5% Conservative: 0
Best Local Similarity: 90.5% Mismatches: 2
Query Match: 93.4% Indels: 20
DB: 2 Gaps: 1

US-10-696-259-6 (1-201) x AAX59348 (1-889)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 66 ATGGCCTGGATGCTGTGCTCATCTTGCATCATGCTCCATCCAGGATCCTGTGCTCTCTGG 125
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 126 GTGTCCCGAGCCCCCTGAGATTGCTACCTGGAAGATCTCTGTGCTTCTGCTGCTGCC 185
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
```

Db 186 TTCATGCGACGACGAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTG 245
 Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValGluAlaProLeu 80
 Db 246 GTTCCAGGAAAGGAGTGGAGTGAATGAAACCCAGAGTTGAG-GGGCGCTGGCCCACTT 304
 Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 305 GCTTCTTCCTCGTTTCTCCATGACACCCAGGCTGAGCTGCACATCCGGGAGCTGGAGGC 364
 Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGly 120
 Db 365 CATGACGCCAGCACTACGTGTCAGAGTGGAGGTGCTGGGCTTGGTGTGGGACAGG 424
 Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyValAlaGlyThrValLeu 140
 Db 425 AATGGAGCTCGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGGTACAGTCTC 484
 Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 Db 485 CTCTTCGGGTGGATTCTATGCTGTGTCAGCTTCTCTGTGGCGGTGGCGAGCACCGTC 544
 Qy 161 TyrTyrGlnGlyLys-Cys----- 166
 Db 545 TATTACCGAGGCAATATGCCAAATCTACTCTCTCCGATTCCCCCAACTCTGAACCTTTC 604
 Qy 167 -----LeuThrTrpLysGlyProArgArgGlnLeuProAlaValProAl 182
 Db 605 CTTCCACCCAGGTCTGACCTGGAAAGTCCAGAGGAGCTGCGGCTGTGTTCCACG 664
 Qy 182 aProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
 Db 665 GCCCTCCACCAACCATGTGGAGCTCAGCACATCTGCTTCCCCAGTCCCGAGGAGGC 722

RESULT 8

AD019809
 ID AD019809 standard; cDNA; 573 BP.
 XX
 AC AD019809;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polynucleotide #367.
 XX
 KW Human; PRO; gene; ss; immune related disorder;
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
 KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 KW renal disease; demyelinating disease; central nervous system;
 KW peripheral nervous system; demyelinating polyneuropathy;
 KW Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 FN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 DR P-PSDB; AD019810.
 XX

PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 1; SEQ ID NO 758; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polynucleotide of
 CC the invention.
 XX
 SQ Sequence 573 BP; 101 A; 168 C; 173 G; 130 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.76e-68 Length: 573
 Score: 876.00 Matches: 173
 Percent Similarity: 90.2% Conservative: 2
 Best Local Similarity: 89.2% Mismatches: 7
 Query Match: 82.1% Indels: 12
 DB: 12 Gaps: 2

US-10-696-259-6 (1-201) x AD019809 (1-573)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
 Db 1 ATGCGCTGGATGCTGTTGCTCATCTTGCATGATGATCCATCCAGATCTGTGCTCTGG 60
 Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
 Db 61 GTGTCCAGGCCCCCTGAGATTCGTACCTTGAAGGATCTCTGCTCTCCCTGCTCTCC 120
 Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 Db 121 TTCAATGCCAGCCCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTCCGAGATGAGGTG 180
 Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValGluAlaProLeu 80
 Db 181 GTTCCAGGAAAGGAGTGGAGNATGGAAACCCAGAGTTCAGGGGCGGCTGGCCCACTT 240
 Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 241 GCTTCTTCCGTTTCTCTCCATGACACCCAGGCTGAGCTGCACATCCGGGACGTGGAGGC 300
 Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGly 120
 Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTGGGACAGG 360
 Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyValAlaGlyThrValLeu 140
 Db 361 AATGGAGCTCGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGGTACAGTCTCTC 420
 Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 Db 421 CTCCTTCGGGCTGGATTCTATGCTGTGTCAGCTTCTCTGTGGCGGTGGGAGCACCGTC 480
 Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
 Db 481 TATTACCGAGGCAAAATGCCACTGTGCATGGGAAACACACTGCCACTCTCAGATGGGCCC 540
 Qy 173 ArgArgGlnLeuProAlaValProAlaProLeuProPro 186
 Db 541 CGA-----GGGTGATTCAGAGCCCAAGATGTCCCC 570

RESULT 9

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AAD06569
ID AAD06569 standard; cDNA; 606 BP.
XX AC
XX AAD06569;
XX DT
XX DT 06-AUG-2001 (first entry)
XX DE
XX DE Human Nkp30 receptor cDNA amplified product.
XX KW
XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
XX KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
XX KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
XX KW therapy; ss.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200136630-A2.
XX PD
XX PD 25-MAY-2001.
XX PF
XX PF 15-NOV-2000; 2000WO-EP011697.
XX PR
XX PR 15-NOV-1999; 99CA-02288307.
XX PR 15-NOV-1999; 99US-00440514.
XX PR
XX PR (INNA-) INNATE PHARMA SAS.
XX PA
XX PA (UYGE-) UNIV GENOVA.
XX PI
XX PI Moretta A, Bottino C, Biassoni R;
XX WPI; 2001-329221/34.
XX DR
XX DR
XX PT
XX PT Novel compound, useful for detection and/or quantifying the presence of
XX PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.
XX PS
XX PS Claim 4; Page 63-64; 83pp; English.
XX CC
XX CC The invention relates to human Nkp30 receptor and its corresponding cDNA
XX CC molecule which is involved in natural cytotoxicity mediated by natural
XX CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX CC useful for detecting and/or quantifying the presence of NK cells in a
XX CC biological sample. The invention also provide kits for detecting and/or
XX CC quantifying the presence of NK cells, for the selective removal of NK
XX CC cells from a biological sample, for the positive and selective
XX CC purification of NK cells from a biological sample and for the in vitro
XX CC stimulation of NK cell cytotoxicity. The invention further provides a
XX CC pharmaceutical composition which is used as a drug for grafting
XX CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
XX CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for
XX CC the prevention, palliation and/or therapy of solid or liquid tumours,
XX CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
XX CC microorganism, notably viral infection. Nkp30 antibodies are useful for
XX CC identifying Nkp30 natural ligands and allow assessment of the level of
XX CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
XX CC comparison of this level to the standard physiological one. Hence Nkp30
XX CC antibodies are useful in the diagnosis of tumours or of infection. The
XX CC present sequence is human Nkp30 receptor cDNA amplified product which is
XX CC obtained by PCR amplification from human Nkp30 receptor cDNA. This
XX CC amplified Nkp30 cDNA product is used for cloning into the pCR2.1 plasmid
XX SQ
XX SQ Sequence 606 BP; 112 A; 180 C; 175 G; 138 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 1.89e-68 Length: 606
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 4 Gaps: 2

US-10-696-259-6 (1-201) x AAD06569 (1-606)

1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTip 20
8 ATGGCTGGATGCTGTGTGCTCATCTTGGTCCATCCAGATCCCTGTCTCTCTGG 67
21 ValSerGlnProProGluThrLeuGluGlySerSerAlaPheLeuProCysSer 40
68 GTGTCCAGCCCTGAGATTCTGACCTGGAGGATCTCTGCTTCTGCTGCTGCTCC 127
41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
128 TTCAATGCCACCAAGGAGACTGGCCATTGGCTCCGTCACTGCTGTTCCGAGATGAGGTG 187
61 ValProGlyLysGluValValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
188 GTTCCAGGGAAGGAGGTGAGGATGGAACCCAGATTCAAGGGCCGCTGGCCCCACTT 247
81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
248 GCTTCTTCCGTTTCTCTCCATGACCACGAGCTGAGCTGCACATCCGGGACGTGCGAGGC 307
101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLysValGlyThrGly 120
308 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGTGTGGGACAGGG 367
121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
368 AATGGGACTCGGCTGGTGGTGGAGAAAGACATCTCTCAGTAGGGGCTGTGTACAGTCTCTC 427
141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
428 CTCCTTCGGGCTGGATTCTATGCTGTGCTCAGCTTTCTCTGTGGCCGTGGGCGAGCACCGTC 487
161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
488 TATTACCAAGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCTCAGATGGGCCC 547
173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
548 CGA-----GGGTGATTCCAGAGCCAGATGTCTCC 577

RESULT 10
AAD06564
ID AAD06564 standard; cDNA; 674 BP.
XX AC
XX AC AAD06564;
XX DT
XX DT 06-AUG-2001 (first entry)
XX DE
XX DE Human Nkp30 receptor cDNA.
XX KW
XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;
XX KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
XX KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
XX KW therapy; ss.
XX OS
XX OS Homo sapiens.
XX FH
XX FH Key
XX CDS
XX CDS 64..636
XX FT
XX FT /*tag= a
XX FT /product= "Human Nkp30 receptor"
XX FT /note= "The coding sequence is specifically claimed as
XX FT SEQ ID NO: 13 in claim 3"
XX FT
XX FT 64..117
XX FT /*tag= b
XX FT 118..633
XX FT /*tag= c
XX FT /product= "Mature human Nkp30 receptor"
XX PN
XX PN WO200136630-A2.
XX PD
XX PD 25-MAY-2001.

```

XX PF 15-NOV-2000; 2000WO-EP011697.
XX PR 15-NOV-1999; 99CA-02288307.
XX PR 15-NOV-1999; 99US-00440514.
XX PA (INNA-) INNATE PHARMA SAS.
XX PA (UYGE-) UNIV GENOVA.
XX FI Moretta A, Bottino C, Biassoni R;
XX DR WPI; 2001-329221/34.
XX DR P-PSDB; AAE02769.
XX PT Novel compound, useful for detection and/or quantifying the presence of
XX PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.
XX PS Claim 3; Page 59; 83pp; English.
XX CC The invention relates to human Nkp30 receptor and its corresponding cDNA
XX CC molecule which is involved in natural cytotoxicity mediated by natural
XX CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor
XX CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
XX CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
XX CC useful for detecting and/or quantifying the presence of NK cells in a
XX CC biological sample. The invention also provide kits for detecting and/or
XX CC quantifying the presence of NK cells, for the selective removal of NK
XX CC cells from a biological sample, for the positive and selective
XX CC purification of NK cells from a biological sample and for the in vitro
XX CC stimulation of NK cell cytotoxicity. The invention further provides a
XX CC pharmaceutical composition which is used as a drug for grafting
XX CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
XX CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for
XX CC the prevention, palliation and/or therapy of solid or liquid tumours,
XX CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
XX CC microorganism, notably viral infection. Nkp30 antibodies are useful for
XX CC identifying Nkp30 natural ligands and allow assessment of the level of
XX CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
XX CC comparison of this level to the standard physiological one. Hence Nkp30
XX CC antibodies are useful in the diagnosis of tumours or of infection. The
XX CC present cDNA sequence encodes human Nkp30 receptor
XX SQ Sequence 674 BP; 124 A; 214 C; 183 G; 152 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.15e-68 Length: 674
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 4 Gaps: 2

US-10-696-259-6 (1-201) x AAD06564 (1-674)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 64 ATGGCTGGATGCTGTTCTCATCTTGATCATGTGTCATCCAGGATCTGTGCTCTCTGG 123

Qy 21 ValSerGlnProGluLeuAlaArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 124 GTGTCCCAAGCCCTCGAGATTCGTACCTCGAAGGATCTCTGCTTCTGCTGCTCC 183

Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 184 TTCATGCCAGCCAGGAGAGACTGGCCATTGGCTCCGTCACGTGTTCCGAGATGAGTG 243

Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 244 GTTCCAGGAAGGAGGTGAGGAATGGAACCCAGAGTTACGGGCCCGCTGCCCCACTT 303

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 304 GCTTCTTCCCGTTTCTCCATGACCAACAGGCTGAGTGCACATCCGGAGCTCGAGGC 363

Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 364 CATGACGCCAGCATCTAGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGGACAGGG 423

Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 424 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGCTAGGGGCTGGTACAGTCTC 483

Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 484 CTCCTTCGGGCTGGATTCTATGCTGTCTCTCTGTGGCCGTGGGAGCAGCACCCGTC 543

Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 544 TATTACAGGGGCAATGCCACTGTCACATGGGAACACACTGCCACTCTCAGATGGGCC 603

Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 604 CGA-----GGRGTGATTCCAGAGCCAGATGTCCC 633

RESULT 11
ADQ59392
ID ADQ59392 standard; DNA; 22173 BP.
XX AC ADQ59392;
XX DT 07-OCT-2004 (first entry)
XX DE Human cancer-associated (CA) gene sequence SEQ ID NO:28.
XX KW human; cancer-associated gene; cancer-associated protein; cytostatic;
XX KW gene therapy; vaccine; tyrosine kinase antagonist;
XX KW G-protein coupled receptor antagonist; cancer; lymphoma; gene; ds.
XX OS Homo sapiens.
XX PN WO2004058288-A1.
XX PD 15-JUL-2004.
XX PF 15-DEC-2003; 2003WO-US040082.
XX PR 17-DEC-2002; 2002US-00322696.
XX PA (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Malandro MS;
XX DR WPI; 2004-543349/52.
XX DR P-PSDB; ADQ59394.
XX PT New cancer-associated nucleic acid for diagnosing, preventing or treating
XX PT cancer (e.g. lymphoma) or for screening agents that may be used for
XX PT treating or preventing cancer.
XX PS Claim 16; SEQ ID NO 28; 143pp; English.
XX CC The present invention describes human cancer-associated (CA) nucleotide
XX CC sequences (1). Also described: (1) an expression vector comprising (1);
XX CC (2) a host cell comprising (1) or the expression vector; (3) a microarray
XX CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
XX CC within an open reading frame of a CA sequence; (5) an isolated antibody,
XX CC or its antigen binding fragment, that binds to the above polypeptide; (6)
XX CC a hybridoma that produces the monoclonal antibody described above; (7) a
XX CC pharmaceutical composition comprising the antibody and a pharmaceutical
XX CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
XX CC the above (monoclonal) antibody or polynucleotide that selectively
XX CC hybridises to any of the polynucleotide sequences mentioned above; (9)
XX CC methods for diagnosing cancer or for detecting the presence or absence of
XX CC cancer cells in an individual; (10) a method for inhibiting growth of
XX CC cancer cells in an individual; (11) a method for delivering a therapeutic
XX CC agent to cancer cells in an individual; (12) an electronic library

CC comprising the polynucleotide or polypeptide, or their fragments;
CC mentioned above; (13) a method of screening for anticancer activity; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC or the presence of the antibody in a test cell or serum sample; (15) a
CC method for screening for a bioactive agent capable of modulating the
CC activity of a CA protein encoded by the above nucleic acid molecule; and
CC (16) a method for treating cancers. (I) has cytostatic activity, and can
CC be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC and as a G-protein coupled receptor antagonist. The compositions and
CC methods of the present invention can be used for diagnosing, preventing
CC and treating cancer, especially lymphomas. They may also be used in
CC screening for agents that may be used for treating or preventing cancer.
CC The present sequence represents a human CA gene sequence, which is given
CC in the exemplification of the present invention. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 22173 BP; 4786 A; 5863 C; 5847 G; 5677 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.36e-66 Length: 22173
Score: 872.00 Matches: 191
Percent Similarity: 52.5% Conservative: 2
Best Local Similarity: 52.2% Mismatches: 172
Query Match: 81.7% Indels: 3
DB: 12 Gaps: 3

US-10-696-259-6 (1-201) x ADQ59392 (1-22173)

QY 3 TrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTyrValSer 22
DB 2577 TGGGTCTTCCTCTG-----CCCCCAGGATCTGTGCTCTCTGGGTGCC 2621

QY 23 GlnProGluLeuLeuLeuLeuGlySerSerAlaPheLeuProCysSerPheAsn 42
DB 2622 CAGCCCCCTGAGATTCGTACCTGGAAGATCTCTGCTTCTGCTGCTCTCTCAAT 2681

QY 43 AlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluValPro 62
DB 2682 GCCAGCAAGGAGAGCTGCCATTGGCTCCGTCACGTGGTTCGAGATGAGTGGTCCA 2741

QY 63 GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
DB 2742 GGGNAGGAGGTGAGGAATGGAAACCCAGAGTTACGGGGCCGCTGGCCCCACTTCTTCT 2801

QY 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisasp 102
DB 2802 TCCCGTTTCTCCATGACACCCAGGCTGAGCTGCACATCCGGGACGTGGAGCCATGAC 2861

QY 103 AlaSerIleTyrValCysArgValGluValLeuGlyValGlyValGlyThrGlyAsnGly 122
DB 2862 GCCAGCATCTAGCTGTGCAGAGTGGAGTGTCTGGGCTTGGTGTGGGACAGGGAATGG 2921

QY 123 ThrArgLeuValValGlu-Lys----- 129
DB 2922 ACTCGGCTGGTGTGGAAAGAGTGAGATGCTGGGAGGTGGTGTCTCTCTGGTGGAG 2981

QY 129 ----- 129
DB 2982 GCCCAAGAGGCAATGTCTTGGGAGGAGGATGCTCTCTGAGGCCCTTCCCTCCCT 3041

QY 130 -----GluHisProGln 133
DB 3042 GAGCCTGTGTGCACTTCTTCCCAACCCCGCTCTCCATTGGCCCCCATGCAATCTCTCA 3101

QY 133 nLeuGlyValGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153
DB 3102 GCTAGGGGCTGGTACAGTCTCTCTCTCGGGCTGGATTCTATGCTGTGAGCTTCTCTC 3161

QY 153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166
DB 3162 TGTGGCCGTGGGAGCACCGTCTATTACCAGGGGCAATGTGATATGGAGCCAGGGGCA 3221

QY 166 ----- 166
DB 3222 ATAGTGGACGGATGGGAGGGGCAGTAAGAGAGTGGGAGGAGGAGGACAGAGACAGGA 3281

QY 166 ----- 166
DB 3282 AGAGGAGAGCCTCGGAGCTGCAACACTGAGCAGCTCTGTGTCTCTGTGACCGGCCAC 3341

QY 166 ----- 166
DB 3342 TGTCAATGGGAACACACTGCCACTCTCAGATGGGCCCGGAGGAGTGTATCCAGAGCCC 3401

QY 166 ----- 166
DB 3402 AGATGTCCCTAGTCTCTTCAAAGAGCCCCAATAAATCTGCCCCACCACTAACTCTCAT 3461

QY 166 ----- 166
DB 3462 GAGTCTCAAGTGTCTTCTTCCATTTCTCCAGATGCCAAATCTACTCTCTCCGATTC 3521

QY 167 -----LeuThrTrpLysGlyProArgArgGlnLeuP 177
DB 3522 CCAACTCTGAACCTTTCCTTCCACAGGTCTGACCTGGAAAGGTCCAAGAGGCGAGTGC 3581

QY 177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProp 197
DB 3582 CGGCTGTGGTCCCGAGCGCCCTCCACCAACATGTGGAGCTCAGCACATCTGCTTCCC 3641

QY 197 roValProGlyGly 201
DB 3642 CAGTCCCGAGGAGGC 3655

RESULT 12
ADZ13655
ID ADZ13655 standard; DNA; 22173 BP.
XX
AC ADZ13655;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated genomic DNA #101.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1175; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal

CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated genomic DNA of
CC the invention.

SQ Sequence 22173 BP; 4785 A; 5863 C; 5847 G; 5678 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.36e-66 Length: 22173
Score: 872.00 Matches: 191
Percent Similarity: 52.5% Conservative: 1
Best Local Similarity: 52.2% Mismatches: 2
Query Match: 81.7% Indels: 172
DB: 14 Gaps: 3

US-10-696-259-6 (1-201) x ADZ13655 (1-22173)

Qy 3 TrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer 22
Db 2577 TGGGTCTTCTCTCG-----CCCCCAGGATCTCTGTCTCTCTGGGTGCC 2621
Qy 23 GlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42
Db 2622 CAGCCCCCTGAGATTCTGACCTCGAAGGATCTCTGCTCTCTGCGCTCTCTCAAT 2681
Qy 43 AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValValPro 62
Db 2682 GCCAGCCAGGGAGACTGGCCATTGGCTCGCTACGTGGTTCAGATGAGGTGTCCA 2741
Qy 63 GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
Db 2742 GGGAGAGAGTGAGGAATGGAACCCAGAGTTTCCAGGGCGCGCTGGCCCATTTGCTTCT 2801
Qy 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
Db 2802 TCCCGTTTCTCTCATGACCCAGCGTGAGCTGCACATCCGGGACGTGCCAGGCGCATGAC 2861
Qy 103 AlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGlyAsnGly 122
Db 2862 GCCAGCATCTACGTGTGCAGAGTGAGGTCTGGGCTTGTGTGGGACAGGGAATGGG 2921
Qy 123 ThrArgLeuValValGlu-Lys----- 129
Db 2922 ACTCGCTGTGTGGTGGAGAAAGTGAGATGTGGGAGGTGTGTCTCTCTCTGGCTGGAG 2981
Qy 129 ----- 129
Db 2982 GCCCAAGAGGCAATGTCTTTGGGAGCGAGGATGTCTCTCTGAGGCCCTTCCCTCCCTC 3041
Qy 130 -----GluHisProG1 133
Db 3042 GAGCTGTGTGCACTTCTTCCCCAACCCCGCTCTCCATTGGCCCCCATCGAACAATCTCA 3101
Qy 133 nLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153
Db 3102 GCTAGGGCTGGTACAGTCTCTCTCTTGGGCTGGATTCTATGCTGTCTGAGTTTCTCTC 3161
Qy 153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166

Db 3162 TGTGGCCGTGGGCGAGCACCGTCTATTACCAGGGCAAATGTGAGTAATGGAGCCAGGGGCA 3221
Qy 166 ----- 166
Db 3222 ATAGTGGACGGGATGGGAGGGCGAGTAAGAGAGTGGGAGGAGGAGGACAGAGACCAGGA 3281
Qy 166 ----- 166
Db 3282 AGAGGAGAGCCTCGGGACTGCAACACTGAGCAGCTCTGTCTCTCTGTGACCAGGCGAC 3341
Qy 166 ----- 166
Db 3342 TGTCAATGGGAACACACTGCCACTCTCAGATGGGCCCCCGAGAGTGAATTCAGAGCC 3401
Qy 166 ----- 166
Db 3402 AGATGTCCCTAGTCTCTTCAAAAGAGCCCCCAATAAATCTGCCCCCACCACCTAATCTCTCAT 3461
Qy 166 ----- 166
Db 3462 GAGTCTCAAGTGTCTTCTCTCCATCTCCAGATGCCAAATCTACTCTCTCCGATTC 3521
Qy 167 -----LeuThrTTrpLysGlyProArgArgGlnLeuP 177
Db 3522 CCAACTCTGAATTTTCCCTTCCACAGGTCTGACCTGGAAGGTCCAAAGAGGAGCGCTGC 3581
Qy 177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProP 197
Db 3582 CGGCTGTGTCTCCAGGCGCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCC 3641
Qy 197 roValProGlyGly 201
Db 3642 CAGTCCAGGAGGC 3655
RESULT 13
ABK84756
ID ABK84756 standard; cDNA; 81800 BP.
XX
AC ABK84756;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #1327.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
XX WO200228999-A2.
XX
XX 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030821.
XX
PR 03-OCT-2000; 2000US-0237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX

PS Claim 1; SEQ ID NO 1327; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GCA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 81800 BP; 19886 A; 19955 C; 20623 G; 21336 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.64e-65 Length: 81800
Score: 872.00 Matches: 191
Percent Similarity: 52.5% Conservative: 1
Best Local Similarity: 52.2% Mismatches: 2
Query Match: 81.7% Indels: 172
DB: 6 Gaps: 3

US-10-696-259-6 (1-201) x ABK84756 (1-81800)

QY 3 TrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer 22
DB 29464 TGGGTCTTCTCTCTG-----CCCCCAGGATCTGTGCTCTCTGGGTGCC 29508
QY 23 GlnProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42
DB 29509 CAGCCCCCTGAGATTCGTACCTGGAGAGATCTCTGCTTCTCTGCCCTGCTCTCAAT 29568
QY 43 AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValPro 62
DB 29569 GCCAGCCAAAGGAGAGCTGCCATTTGGCTCCGTCACGTGTCCTCCGAGATGAGGTGGTTCCA 29628
QY 63 GlyIleGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
DB 29629 GGGAAAGGAGGTAGAGAAATGGAAACCCAGAGTTTCAGGGGCGGCTGGCCCCACTTCTTCT 29688
QY 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
DB 29689 TCCCGTTTCTTCATGACACACAGCTGAGCTGACATCCGGGCGTGGAGGCCATGAC 29748
QY 103 AlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGlyAsnGly 122
DB 29749 GCCAGCATCTACGTGTCAGAGTGGAGGTGCTTGGGCTTGGGTGTCGGGACAGGGAATGG 29808

QY 123 ThrArgLeuValValGlu-Lys----- 129
DB 29809 ACTCGCTGTGTGTGGAGAAAGTGTGATGCTGGGAGGTGGTGTCTCTCTCTGGCTGGAG 29868
QY 129 ----- 129
DB 29869 GCCCAAGAGGCAATGCTCTTGGGAGGAGGATGCTCTCTGAGGCCCTTCCCTCCCT 29928
QY 130 -----GluHisProG1 133
DB 29929 GAGCCTGTGTGCACTTCTTCCCAACCCCGCTCTCCATTGCCCATGCGAAGACCTCTCA 29988
QY 133 nleuGlyValaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153
DB 29989 GCTAGGGGCTGGTACAGTCTCTCTCTCGGCTGGATTCTATGCTGTGACGCTTCTCTC 30048
QY 153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166
DB 30049 TGTGGCGGTGGGCGAGCACCGCTCTATTACAGGGCAATGTGATTAATGGAGCCAGGGGCA 30108
QY 166 ----- 166
DB 30109 ATAGTGCACGGGATGGGAGGGGCGAGTAAGAGAGTGGAGGAGGAGGACAGACCAGGA 30168
QY 166 ----- 166
DB 30169 AGAGGAGAGCCTCGGAGCTGCAACACTGAGCAGCTCTGTCTCTCTGACCAGGCCAC 30228
QY 166 ----- 166
DB 30229 TGTACATGGGAACACACTGCCACTCTCTCAGATGGGCGCCGAGGAGTGTATTCAGAGCCC 30288
QY 166 ----- 166
DB 30289 AGATGTCCCTAGTCTCTTCAAAAGACCCCAATAATCTGCCCCACCACTAATCTTCAT 30348
QY 166 ----- 166
DB 30349 GAGTCTCAAGTGTCTTCTCTCCATTCTCCAGATGCCAAATCTACTCTCTCCGATTCCC 30408
QY 167 -----LeuThrTrpLysGlyProArgArgGlnLeuP 177
DB 30409 CCAACTCTGAACCTTTCCTTCCACCAGGTCTGACCTGGAAAGGTCCAAGAGGCGAGTGC 30468
QY 177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProP 197
DB 30469 CGGCTGTGTTCCCGAGCGCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCC 30528
QY 197 roValProGlyGly 201
DB 30529 CAGTCCCAGGAGGC 30542
RESULT 14
ID ADW38506/c
ID ADW38506 standard; cDNA; 6853 BP.
XX AC ADW38506;
XX XX
DT 24-MAR-2005 (first entry)
XX XX
DE Immunomodulatory gene LST-1 cDNA.
XX KW cytostatic; immunosuppressive; virucide; diagnosis; prognosis;
KW pharmaceutical; immunotherapy; cancer; cytostatic; neoplasm;
KW autoimmune disease; immunosuppressive; immune disorder; viral infection;
XX KW infection; LST-1; gene; ss.
XX OS Homo sapiens.
XX XX
PN WO2005000099-A2.
XX XX
PD 06-JAN-2005.

XX 09-JUN-2004; 2004WO-US018461.
 XX 09-JUN-2003; 2003US-0477291P.
 XX (GENZ) GENZYME CORP.
 XX Roberts BL;
 XX WPI; 2005-058046/06.
 XX P-PSDB; ADW38505.
 XX New isolated blood factor domain polynucleotides having immunomodulatory
 PT activity, useful for aiding in the diagnosis or treating disorders
 PT relating to the immune responses, e.g. cancers, autoimmune diseases, or
 PT viral infections.
 XX Disclosure; SEQ ID NO 15; 141pp; English.
 XX The invention describes an isolated polynucleotide (I) encoding a peptide
 CC selected from 21 polynucleotides fully given in the specification, or the
 CC complement of the polynucleotide. Also described are: an isolated peptide
 CC selected from 21 peptides fully given in the specification; a host cell
 CC comprising (I) or the peptide; an antibody that specifically recognizes
 CC and binds the peptide; a composition comprising the host cell, the
 CC peptide, or the antibody, and a pharmaceutical carrier; an immune
 CC effector cell raised in the presence and at the expense of a host cell;
 CC and a method for eliciting a cytolytic response in a subject. Also
 CC disclosed are: a method for monitoring gene expression; a method for
 CC modulating the expression of the immunomodulatory polynucleotides and
 CC expression products; a method for screening for candidate agents that
 CC modulate the expression of the polynucleotide or the expression products
 CC of the polynucleotide; assays for the identification, assessment, and
 CC development of candidate agents capable of modulating the activity of the
 CC polynucleotides or polypeptides; a method for monitoring an immune
 CC response in a subject; and a method for active immunotherapy. The
 CC polynucleotides (e.g., blood factor domains) having immunomodulatory
 CC activity are useful for detecting, diagnosing, prognosing, or monitoring
 CC the progression of a disease. They are useful for aiding in the diagnosis
 CC or treating disorders relating to the immune responses, e.g. cancers,
 CC autoimmune diseases, or viral infections. This sequence encodes
 CC immunomodulatory gene LST-1 membrane receptor alternative spliced soluble
 CC form.
 XX SQ Sequence 6853 BP; 1798 A; 1724 C; 1832 G; 1499 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3.52e-65 Length: 6853
 Score: 853.50 Matches: 186
 Percent Similarity: 52.7% Conservative: 0
 Best Local Similarity: 52.7% Mismatches: 0
 Query Match: 80.0% Indels: 167
 DB: 14 Gaps: 2
 US-10-696-259-6 (1-201) x ADW38506 (1-6853)
 Qy 16 SerCysAlaLeuTrrpValSerGlnProGluIleArgThrLeuGluGlySerSerAla 35
 Db 5220 TCTGTGCTCTCTGGGTGTCAGAGTTCGATTCCTCCAGGAGATCTCTGCCC 5161
 Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
 Db 5160 TTCCTGCCCTGCTCTTCAATGCCAGCCAGGAGACTGGCCATTGGCTCCGTCACGTGG 5101
 Qy 56 PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly 75
 Db 5100 TTCCGAGATGAGTGGTTCACAGGGAAGGAGGTGAGGAATGAAACCCAGAGTTGAGGGC 5041
 Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
 Db 5040 CGCTGGCCCCACTTGTCTTCCCGTTCTCTCATGACCCAGGCTGAGCTGCACATC 4981
 Qy 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeu 115

Db 4980 CCGGACCTGGCAGGCCCATGACGCCAGCATCTACGTGTGCAGAGTGGAGTCTGGCCCTT 4921
 Qy 116 GlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys----- 129
 Db 4920 GGTGTGGGACAGGGAATGGGACTCGGCTGTGTGGTGGAGAAAGGTGAGATCTGGGAGGT 4861
 Qy 129 ----- 129
 Db 4860 GGTGTCTCTCTCTGGTGGAGGCCCAAGAGGCAATGTCTTGGGAGGAGGATGTCTCC 4801
 Qy 129 ----- 129
 Db 4800 TCTGAGGCCCTTCTCTCTCTGAGCCCTGTGTGCATCTTCTTCCCAACCCCGTCTCCATT 4741
 Qy 130 -----GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPhe 146
 Db 4740 GCCCATGCGAGAACATCTCTAGCTAGGGGCTGGTACAGTCTCTCTCTCTGGGTGGATT 4681
 Qy 146 eTyrAlaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysC 166
 Db 4680 CTATGCTGTGAGCTTTCTCTCTGTGGCGGTGGGCGAGCACCGTCTATTACAGGSCAATG 4621
 Qy 166 s----- 166
 Db 4620 TGAGTAATGGAGCCAGGGGCAATAGTGGACGGGATGGGGGCGAGTAAGAGAGTGGGAG 4561
 Qy 166 ----- 166
 Db 4560 GAGGAGGACAGAGACCCAGGAAGAGAGAGACCTCGGGAGTGCACACTGAGCAGCTCCTG 4501
 Qy 166 ----- 166
 Db 4500 TCCTCTCTTGACCAGGCCACTGTACATGGGAACACACTGCCACTCTCTCAGATGGGCC 4441
 Qy 166 ----- 166
 Db 4440 CGAGGAGTGTATTCAGAGCCAGATGTCCCTAGTCTCTTCAAAGACCCCAATAATCT 4381
 Qy 166 ----- 166
 Db 4380 GCCCCACCACTAATCTCATGAGTCTCAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 4321
 Qy 167 -----LeuThrTrpL 170
 Db 4320 ATCTACTCTCTCCGATTTCCCACTCTGAACTTTTCCCTTCCACACAGGTCTGACCTGGA 4261
 Qy 170 YsGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProProCysGly 190
 Db 4260 AAGGTCCAAGAGGAGCTGCGGCTGTGGTCCAGGCGCCCTCCACACCACCATGTGGGA 4201
 Qy 190 erSerAlaHisLeuLeuProProValProGlyGly 201
 Db 4200 GCTCAGCACATCTGCTTCCCTCCAGGAGGC 4166
 RESULT 15
 ID AAX59347
 ID AAX59347 standard; cDNA; 671 BP.
 XX AAX59347;
 AC AAX59347;
 XX 20-SEP-1999 (first entry)
 DT XX
 DE Human B-cell myelin oligodendrocyte glycoprotein BMOG cDNA.
 XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
 KW signal transduction; immunomodulator; antiinflammatory;
 KW autoimmune disease; inflammation; gene therapy; diagnosis; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Key 66. .637
 FT CDS

```
FT      /*tag= a
FT      /transl_except= (pos:291..292, aa:Arg)
FT      /note= "this codon contains an apparent 1 nucleotide
FT      deletion, which alters the reading frame"
FT      66..101
FT      sig_peptide
FT      /*tag= b
FT      mat_peptide
FT      102..634
FT      /*tag= c
XX
PN      WO9923867-A2.
XX
PD      20-MAY-1999.
XX
PF      05-NOV-1998; 98WO-US023826.
XX
PR      07-NOV-1997; 97US-0064761P.
XX
PA      (BIOJ ) BIOGEN INC.
XX
PI      Browning J;
XX
XX      WPI; 1999-418423/35.
DR      P-PSDB; AAY06401.
XX
XX      Novel B-cell myelin oligodendrocyte glycoproteins.
XX
PS      Claim 1; Page 40; 43pp; English.
XX
XX      This DNA sequence encodes human BMOG, a novel member of the B cell myelin
XX      oligodendrocyte glycoprotein family that is expressed by germinal centre
XX      B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
XX      identified. The protein is present primarily in the spleen, in lymph
XX      nodes and in germinal centre B cells. It may have immunoregulatory
XX      functions, and soluble or chimeric fusion proteins of BMOG may be used to
XX      regulate the immune system in autoimmune or inflammatory disease. Vectors
XX      comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
XX      producing BMOG using these transformed host cells are also provided. BMOG
XX      polypeptides can be used for modulating the immune system of a subject or
XX      to inhibit signal transduction in a cell expressing BMOG by contacting it
XX      with a soluble BMOG protein. The nucleic acid can be used for gene
XX      therapy. The protein can also be used to target a toxin, imaging agent or
XX      radionuclide to a cell expressing BMOG. (All claimed.)
XX
SQ      Sequence 671 BP; 124 A; 211 C; 184 G; 152 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.46e-66 Length: 671
Score: 848.00 Matches: 172
Percent Similarity: 89.7% Conservative: 2
Best Local Similarity: 88.7% Mismatches: 8
Query Match: 79.5% Indels: 13
DB: 2 Gaps: 2

US-10-696-259-6 (1-201) x AAX59347 (1-671)

QY      1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
DB      66 ATGGCGCTGGATGCTGTGCTCATCTTGATCATGGTCCATCCAGGATCCTGTGCTCTGG 125
QY      21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
DB      126 GTGTCCAGCCCCCTGAGATTCGTACCTCGTGAAGGATCCTCTGCTCTGCGCTGCTCC 185
QY      41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluVal 60
DB      186 TTCAATGCCAGGCAAGGGAGACTGGCCATTGGCTCCGTCCATCCAGGATTCAGTGGGTTG 245
QY      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
DB      246 GTTCCAGGGAGAGGTGAGGATGGAAACCCAGAGTTTCAG-GGGCGCTGGCCCCACTT 304
QY      81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
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Db      305 GCTTCTTCCCGTTTCTCCTCCATGACCACCAGGCTGAGCTGCACATCCGGGACGTGCCAGGC 364
QY      101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
DB      365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTCCGGACAGGG 424
QY      121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
DB      425 AATGGGACTCGGCTGGTGGTGAGAAACATCCTCAGCTAGGGGCTGGTACAGTCTCTC 484
QY      141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
DB      485 CTCCTTCGGGCTGGATTCTATGCTGTGCTTCTCTGTGGCCCTGGGCGACACCGTC 544
QY      161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
DB      545 TATTACAGGGCAATGCCACTGTACATGGGAACACACTGCCCACTCTCAGATGGGCC 604
QY      173 ArgArgGlnLeuProAlaValValProAlaProAlaProLeuProPro 186
DB      605 CGA-----GGAGTGATTCCAGAGCCAGAGATGTCCC 634
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Search completed: February 28, 2006, 09:14:55
Job time : 600 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 06:33:58 ; Search time 3876 Seconds
(without alignments)
2426.265 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAMWLLILIVHFGSCALW.....APLPFGCSAHLPPVPGG 201

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORES=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs07
-USER=US10696259 @CGN 1 1 5315 @runat_27022006_123556_27156 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hcc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1025	96.1	1087	4 BC018752	BC018752 Homo sapi
2	1015	95.1	1052	3 BM561738	BM561738 AGENCOURT
3	1004	94.1	878	2 BG745027	BG745027 602723117
4	988	92.6	841	3 BM561953	BM561953 AGENCOURT
5	988	92.6	1040	3 BQ053062	BQ053062 AGENCOURT
6	906	84.9	949	3 BQ053083	BQ053083 AGENCOURT
7	876	82.1	573	11 DQ052145	DQ052145 Homo sapi

8	869	81.4	573	11	DQ052146	DQ052146 Pan trogl
9	861.5	80.7	978	2	BG744192	BG744192 602722992
10	845.5	79.2	913	2	BG341330	BG341330 602463806
11	841	78.8	741	2	BG744854	BG744854 602722992
12	706.5	66.2	809	2	BG744382	BG744382 602723117
13	653	61.2	637	2	BG398004	BG398004 602439532
14	643	60.3	574	3	BM363549	BM363549 BS320057A
15	620	58.1	719	1	AW967444	AW967444 EST379519
16	593	55.6	541	3	BM364334	BM364334 BS3100020
17	578	54.2	523	3	BM364807	BM364807 BS3200050
18	557	52.2	508	3	BM364361	BM364361 BS3100020
19	534	50.0	505	6	CB428714	CB428714 604459 MA
20	516.5	48.4	451	1	AA262074	AA262074 z821a05.s
21	487	45.6	980	3	BQ053262	BQ053262 AGENCOURT
22	482	45.2	503	5	BX283861	BX283861 BX283861
23	478	44.8	501	5	BX283089	BX283089 BX283089
24	458	42.9	440	1	AA846055	AA846055 ak79e02.s
25	398	37.3	505	3	BM088311	BM088311 501749 MA
26	395	37.0	872	3	BQ053092	BQ053092 AGENCOURT
27	390	36.6	353	6	CB428376	CB428376 604075 MA
28	390	36.6	1639	3	BM917537	BM917537 AGENCOURT
29	378	35.4	492	1	AA237100	AA237100 z801h06.r
30	351	32.9	471	1	AA894045	AA894045 EST197848
31	327	30.6	379	1	AA236886	AA236886 z801h06.s
32	289	27.1	308	2	BF522619	BF522619 UI-R-C3-s
33	287	26.9	374	7	CR464436	CR464436 CR464436
34	283.5	26.6	480	1	AV599289	AV599289 AV599289
35	268	25.1	354	1	AI511264	AI511264 UI-R-C3-s
36	256	24.0	282	1	BM308336	BM308336 3497 MARC
37	228	21.4	311	1	AW971514	AW971514 EST383603
38	185	17.3	182	1	AA721754	AA721754 nx82d04.s
39	144.5	13.5	630	1	AL878396	AL878396 AL878396
40	144.5	13.5	739	8	DR850889	DR850889 JGI_CABE1
41	144.5	13.5	803	8	DN098981	DN098981 JGI_CABE8
42	144.5	13.5	861	8	CX747707	CX747707 JGI_AHP6
43	143	13.4	1089	10	CL037400	CL037400 CHZ16-43D
44	137.5	12.9	690	5	BX773925	BX773925 BX773925
45	136.5	12.8	560	2	BE371457	BE371457 601223157

ALIGNMENTS

BC018752	1087 bp	mRNA	linear	HTC 19-NOV-2003
BC018752	Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cdna			
Clone IMAGE:4849421), containing frame-shift errors.				
BC018752	GI:17511805			
HTC				
Homo sapiens (human)				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
Hominidae; Homo.				
1 (bases 1 to 1087)				
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,				
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,				
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,				
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heiseh,F.,				
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,				
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,				
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,				
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,				
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,				
McKernan,R.J., Malek,J.A., Gunaratne,P.H., Richards,S.,				
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,				
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,				
Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,				
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,				
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,				
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,				
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,				


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QY 160 lTyrTrpGlnGlyys-Cys----- 166
Db 296 CTATTACAGGCAATATATGCAAAATCTACTCTCCGGATTCCCCCAACTCTGAACCTT 237

QY 167 -----LeuThrTrpGlyProArgArgGlnLeuProAlaValValProA 182
Db 236 CCCTTCCACCAGGTCTCAGCTGGAAAGGTCAAGAAGGAGTCGCGGCTGGTCCAG 177

QY 182 laProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 176 CGCCCTCCACCACCATGTTGGGAGCTCAGCACATCTGTTCCCCAGTCCAGGAGGC 118

RESULT 4
BM561953 841 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6593188 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484506
DEFINITION 5', mRNA sequence.
ACCESSION BM561953
VERSION BM561953.1 GI:18807631
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 841)
NIH-MGC http://mnc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2013 row: o column: 03
High quality sequence stop: 641.
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            /clone="IMAGE:5484506"
            /tissue_type="natural killer cells, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 106"
            /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1,54e-82 Length: 841
Score: 988.00 Matches: 193
Percent Similarity: 90.6% Conservative: 0
Best Local Similarity: 90.6% Mismatches: 1
Query Match: 92.6% Indels: 19
DB: 3 Gaps: 1

US-10-696-259-6 (1-201) x BM561953 (1-841)

QY 8 lIleuIleMetValHisProGlySerCysAlaLeuThrValSerClnProGluIle 27
Db 3 ATCTTGATCATGTCATCCAGGATCTGTGCTCTCTGGTGTCCAGCCCTTGAGATT 62

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QY 28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg 47
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QY 48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg 67
Db 123 CTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTGGTTCCAGGGAAGGAGGTGAGG 182

QY 68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis 87
Db 183 AATGGAAACCCAGAGTTACGGGGCGCTGGCCCACTTCTTCTTCCCGTTTCTTCAT 242

QY 88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrVal 107
Db 243 GACCACCAAGCTGAGCTGCACATCCGGACGTGGAGGCCATGACGCCAGCATCTACGTG 302

QY 108 CysArgValGluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValVal 127
Db 303 TGCAGAGTGGAGGTGCTGGGCTTGGTGTCCGGACAGGGAATGGGACTCGGCTGGTGGTG 362

QY 128 GluLysGluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyr 147
Db 363 GAGAAAGAAATCTCAGCTAGGGGCTGGTACAGTCTCTCTTCCGGCTGGATTCTAT 422

QY 148 AlaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLys-Cys-- 166
Db 423 GCTGTGAGCTTCTCTCTGTGGCGGTGGCAGCACCGCTATTACCAGGGCAATATATGCC 482

QY 167 -----LeuThrTyr 169
Db 483 AAATCTACTCTCTCCGGATTCCCACTCTGAACTTTCCTTCCACCAAGTCTGACCTG 542

QY 169 pLysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProCysGly 189
Db 543 GAAAGGTCACAGGAGGAGGCTGCCGCTGTGGTCCAGCGCCCTCCACCAACCATGTGG 602

QY 189 YSerSerAlaHisLeuLeuProProValProGlyGly 201
Db 603 GAGCTCAGCACATCTGCTTCCCCAGTCCCAGGAGGC 639

RESULT 5
BM561953 1040 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT_6821798 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5934616
DEFINITION 5', mRNA sequence.
ACCESSION BM561953
VERSION BM561953.1 GI:19812402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1040)
NIH-MGC http://mnc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2121 row: a column: 17
High quality sequence stop: 748.
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/clone_lib="NIH_MGC_106"
/notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

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Alignment Scores:
Pred. No.:      2,01e-82      Length:      1040
Score:          988.00      Matches:      193
Percent Similarity: 90.6%      Conservative: 0
Best Local Similarity: 90.6%      Mismatches: 1
Query Match:      92.6%      Indels:      19
DB:              3          Gaps:      1
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US-10-696-259-6 (1-201) x BQ053062 (1-1040)

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Qy 8 IleLeuIleMetValHisProGlySerCysAlaLeuTrpValSerGlnProProGluIle 27
    |||||
Db 2 ATCTTGATCATGGTCCATCCAGGATCTGTCTCTGGGTGTCCAGCCCCCTGAGATT 61

Qy 28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg 47
    |||||
Db 62 CGTACCTTGGAGGATCTCTGCCTCTCTGCCTCTCTCAATGCCAGGAGGAGA 121

Qy 48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLyValArg 67
    |||||
Db 122 CTGGCCATGGTCCGTCACGTGGTTCGAGATGAGGTGGTTCAGGAGAGAGTGAGG 181

Qy 68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis 87
    |||||
Db 182 AATGGAACCCAGAGTTTCAGGGGCGCTGGCCCCACCTTGCTTCTTCCCGTTTCTCCAT 241

Qy 88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTrpVal 107
    |||||
Db 242 GACCACGAGGTGAGTGCATCCGGGACGTCGGAGGCCATGACGCCAGCATCTACGTG 301

Qy 108 CysArgValGluValLeuGlyValGlyThrGlyAenGlyThrArgLeuValVal 127
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Db 302 TGCAGAGTGGAGGTGCTGGGCTTGGTTCGGGACAGGGAATGGACTCGGCTGGTGGTG 361

Qy 128 GluLySGLuHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuAlaGlyPheTrp 147
    |||||
Db 362 GAGAAAGAACATCTCAGTAGGGGCTGGTACAGTCTCTCTCTTGGGCTGGATTCTAT 421

Qy 148 AlaValSerPheLeuSerValAlaValGlySerThrValTrpThrGlnGlyLys-Cys-- 166
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Db 422 GCTGTACGCTTTCTCTCTGTGGCGTGGGACAGCACCGTCTATTACAGGGGAAATATGCC 481

Qy 167 -----LeuThrTr 169
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Db 482 AAATCTACTCTCTCGGANTCCCCAACTCTGAATTTCCCTTCCACGAGTCTGACCTG 541

Qy 169 pLySGLyProArgArgGlnLeuProAlaValValProAlaProLeuProProCysG1 189
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Db 542 GAAAGTCCAGAGAGGAGCTGCGGCTGTGGTCCAGGGGCCCTTCCACCAACCATGTGG 601

Qy 189 ySerSerAlaHisLeuLeuProProValProGlyGly 201
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RESULT 6

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LOCUS      BQ053083      949 bp      mRNA      linear      EST 29-MAR-2002
DEFINITION AGENCOUNT_6821591 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5934651
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BQ053083
BQ053083.1 GI:19812423
EST.
Homo sapiens (human)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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REFERENCE

1 (bases 1 to 949)

NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM2121 row: c column: 04

High quality sequence stop: 549.

FEATURES

source

Location/Qualifiers

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/notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Alignment Scores:

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Score:          905.00      Matches:      184
Percent Similarity: 92.5%      Conservative: 2
Best Local Similarity: 91.5%      Mismatches: 13
Query Match:      84.9%      Indels:      3
DB:              3          Gaps:      0
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US-10-696-259-6 (1-201) x BQ053083 (1-949)

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Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
    |||||
Db 268 GTGTCCAGGCCCTTGAGATTGCTTACCTGGAAGGATCCTTGCTTCTGCTGCTGCTCC 327

Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
    |||||
Db 328 TTCATGCCAGCCAGGAGGAGACTGGCCATTTGGCTCCGTCCAGTGGTTCGAGATGAGGTG 387

Qy 61 ValProGlyLySGLuValArgAenGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
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Db 388 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCCCGCTGGCCCACTT 447

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
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Db 448 GCTTCTTCCCGTTTCTCTCCATGACCCACAGGCTGAGCTGCACATCCGGGACGTGCGAGGC 507
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Qy 101 HispAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
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Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrVal-Le 140
Db 568 AATGGGACTCGCTGGTGGTGGAGAAAGAACATCCTCAGCTTANGGGCTGGTACAGTCCCT 627
Qy 140 uLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVa 160
Db 628 CCYCCITTCGGGCTGGATTCATGCTGTGAGCTTTCTCTGTGGCCGTGGGACACCGT 687
Qy 160 lTyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLeuProAlaValVa 180
Db 688 CTATTACAG-GGCNAATGTCTGACCTGAAAAGGTCAAAGGCGAGCTGCCCGGTGTGTT 746
Qy 180 lProAlaProLeuProProProCys-GlySerSerAlaHisLeuLeuProProValPro 199
Db 747 CCCAAGGGCCCTCCACCAACATGTTGGAGCTCACACAATCTGTTCCCGCCAGTCCC 805

RESULT 7
LOCUS DQ052145 573 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens NCR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ052145
VERSION DQ052145.1 GI:66905601
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE 1 (bases 1 to 573)
JOURNAL (er) F10S Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source Location/Qualifiers
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gene
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ORIGIN
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Pred. No.: 876.00 Matches: 173
Score: 90.2% Conservative: 2
Percent Similarity: 89.2% Mismatches: 7
Best Local Similarity: 82.1% Indels: 12
Query Match: 11 Gaps: 2
DB:

US-10-696-259-6 (1-201) x DQ052145 (1-573)
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Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCACGCCAGGAGACTGGCCATTGGCTCCGTACAGTGGTTTCCGAGATGAGGTG 180
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCCAGGGAGAGGAGGTGAGGAATGGAACCCAGAGTTCAGGGGGCCCTTGGCCCCACTT 240
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCTTCTTCCGTTTCTCCATGACCCAGGCTGAGCTGCACATCCGGGACGTGCGAGGC 300
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGCAGGTGCTGGCCCTTGGTGTGCGGACAGGG 360
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGCTGGTGGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTCTCTC 420
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGAATTCATGCTGTGAGCTTTCTCTGTGGCCGTGGGACGACCGTC 480
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACCGGGCAATGCCACTGTGCATGGGAACACACTGCCACTCCTCAGATGGGCC 540
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 541 CGA-----GGAGTGATTCCAGAGCCAGCATGTGCC 570

RESULT 8
LOCUS DQ052146 573 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes NCR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ052146
VERSION DQ052146.1 GI:66905602
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) F10S Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source Location/Qualifiers
1..573
/organism="Pan troglodytes"

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gene
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>573
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/locus_tag="HC20172"

ORIGIN

Alignment Scores:
Pred. No.: 1.5e-71 Length: 573
Score: 869.00 Matches: 172
Percent Similarity: 89.7% Conservative: 2
Best Local Similarity: 88.7% Mismatches: 8
Query Match: 81.4% Indels: 12
DB: 11 Gaps: 2

US-10-696-259-6 (1-201) x DQ052146 (1-573)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCCTGGATGCTGTGCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCGG 60
Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCTCGATTCGTACCTCGAAGATCCTCTGCTTCTCTGCTCTGCTCC 120
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTCGTTCCGAGATGAGGTG 180
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCCAGGGAAGGAGGTGAGAAATGAACCCCGAGTTTCAGGGCGCGCTCGGCCACTT 240
Qy 81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCTTCTTCCGTTTCTTCATGACACACAGCTGAGCTGACATCCGGGAGCTGCGAGGC 300
Qy 101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGCGGACAGG 360
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGTGACAGTCCCTC 420
Qy 141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGATTCTATGCTGTACGCTTCTCTGTGGCCGTGGGCGACGCCGTC 480
Qy 161 TyrTyrrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACCAGGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCCTCAGATGGGCC 540
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 541 CGA-----GGAGTGTATTCAGAGCCAGAGGTCCC 570

RESULT 9
BG744192 978 bp mRNA linear EST 15-MAY-2001
LOCUS 60272292F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849222 5',
DEFINITION mRNA sequence.
ACCESSION BG744192
VERSION BG744192.1 GI:14054845
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@b-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCMI688 row: h column: 23
High quality sequence stop: 802.
Location/Qualifiers
1..978

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849222"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 106"
/note="Organ: blood, Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.5e-70 Length: 978
Score: 861.50 Matches: 172
Percent Similarity: 86.3% Conservative: 4
Best Local Similarity: 84.3% Mismatches: 21
Query Match: 80.7% Indels: 7
DB: 2 Gaps: 3

US-10-696-259-6 (1-201) x BG744192 (1-978)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCCTGGATGCTGTGCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCGG 324
Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCAGGCCCTCGATTCGATTCGAGGATCCTCTGAGGATCCTCTGCTCTGCTCTGCTCC 384
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCAATGCCAGCCAGGAGGAGACTGGCCATTGGCTCCGTCAGTGTTCGAGATGAGGTG 444
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCCAGGGAAGGAGGTGAGAAATGGGACCCAGAGTTTCAGGGCGCGCTGGCCCACTT 504
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTTCCGCTTTCCTCCATGACACACAGCTGAGCTGCACATCCGGGAGCTGCGAGGC 564
Qy 101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 565 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGCGGACAGG 624
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGTGATCAGTCTCTC 684
Qy 141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 685 CTCCTTCGGGCTGGATTCTATGCTGTGCTGCTCTCTCTGTGAGCGGTGGGCGACGCCGTC 744

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QY 161 TTTTCTGlnGlyLysCysLeuThrTrpLys-----GlyProArgArgGlnLeuProAla 178
Db 745 TATTACGAGCAATATGCCAAATCTACTCTCTCGATTCCTCCCAATCTGAATCTCCCTCC 804
QY 179 ValVal---ProAlaProLeuProProCys-----GlySerSerAlaHis 193
Db 805 ACGGTCTGACCTGGAAGTCCAGAGCGAGTGCGGTGTGGCCAGGCGCTCCCAACAC 864
QY 194 LeuLeuProPro 197
Db 865 ATGTGGGAGCCA 876

RESULT 10
BG341330 913 bp mRNA linear EST 27-FEB-2001
LOCUS 602463806F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576657 5',
DEFINITION mRNA sequence.
ACCESSION BG341330
VERSION BG341330.1 GI:13147768
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 913)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1289 row: 1 column: 02
High quality sequence stop: 781.
FEATURES
Location/Qualifiers
1..913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4576657"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pONB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4,4e-69 Length: 913
Score: 845.50 Matches: 180
Percent Similarity: 82.4% Conservative: 2
Best Local Similarity: 81.4% Mismatches: 11
Query Match: 79.2% Indels: 30
DB: 2 Gaps: 2

US-10-696-259-6 (1-201) x BG341330 (1-913)

QY 9 LeuLeuMetValHisProGly-----SerCysAlaLeu 19
Db 60 TTGATGCTCGAGGTCCTCGGAGTTGTGTCTCTGGCAAGTGATGTGATCTCTGCTCTC 119

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QY 20 TrpValSerGlnProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCys 39
Db 120 TGGGTGTCCAGCCCTGAGATTCGACCTCGAAGGATCTCTGCTTCTGCTTCTGCTGCTGC 179
QY 40 SerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGlu 59
Db 180 TCCTTCAATGCCAGCAAGGAGGACTGGCCATTGGCTCCGTCACGTGTGTTCCGAGATGAG 239
QY 60 ValValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaPro 79
Db 240 GTGGTTCCAGAAAG-GAGGTGAGGAATGGAAACCCAGAGTTCAGGTGCCCTCCGCCCA 298
QY 80 LeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArg 99
Db 299 CTTGCTTCTTCCCGTTTCTCCATGACCACAGGCTGAGCTGCACATCCGGAGCTGCGA 358
QY 100 GlyHisAspAlaSerIleThrValCysArgValGluValLeuGlyLeuGlyValGlyThr 119
Db 359 GGCCATGACGCCAGCATCTACGTGTGCAGAGTGAGGTGCTGGGCTTGGTGTGCGGACA 418
QY 120 GlyAsnGlyThrArgLeuValValGlyLysGluHisProGlnLeuGlyAlaGlyThrVal 139
Db 419 GGGAAATGGGACTCGGCTGGTGGTGGAGAAACATCTCAGCTAGGGGCTGGTACAGTC 478
QY 140 LeuLeuLeuArgAlaGlyPheThrAlaValSerPheLeuSerValAlaValGlySerThr 159
Db 479 CTCCTCTCTGGGCTGGATCTATGCTGTGAGCTTCTCTGTGGCGCTGGGAGCACC 538
QY 160 ValTrpTrpGlnGlyLys----- 165
Db 539 GTCTATTACCAGGCAAAATATATGCAATCTACTCTCCGATCCCAATCTCAACTTT 598
QY 166 -----CysLeuThrTrpLysGly-ProArgArgGlnLeuProAlaValValPr 181
Db 599 CCCTTCCACCAGGCTCTGGACCTGGACAGTCCCAAGGAGGAGCTGCGGCTGGTCCC 658
QY 181 oAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyVGL 201
Db 659 AGCCCTCTCCACCACACA-AGTGGAGCTGAGCACATCTGCTTCCCCCAGTCCAGGAGG 717
QY 201 Y 201
Db 718 T 718

RESULT 11
BG744854/c 741 bp mRNA linear EST 15-MAY-2001
LOCUS 602722992T1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849222 3',
DEFINITION mRNA sequence.
ACCESSION BG744854
VERSION BG744854.1 GI:14055507
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 741)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1688 row: h column: 23
High quality sequence stop: 741.

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FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:484922"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 8,95e-69 Length: 741
Score: 841.00 Matches: 165
Percent Similarity: 89.2% Conservative: 0
Best Local Similarity: 89.2% Mismatches: 1
Query Match: 78.8% Indels: 19
DB: 2 Gaps: 1

US-10-696-259-6 (1-201) x BG744854 (1-741)

Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
Db 741 TTCCTGCCCTCTCTCTCAATGCCAGCCAGGGAGCTGGCCATTTGGCTCCGTCACGTGG 682
Qy 56 PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly 75
Db 681 TTCGAGATGAGTGGTTCAGGGAGAGAGTGGAGATGGAACCCAGAGTTACGGGCG 622
Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
Db 621 CGCCTGGCCCACTTGCTTCTCCGTTTCTCCATGACCACCGAGCTGAGCTGCACATC 562
Qy 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeu 115
Db 561 CGGACGTCGAGGCCATGACGCCAGCATCTACGCTGTCAGAGTGGAGTCTGGGCGCTT 502
Qy 116 GlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGly 135
Db 501 GGTGTGGGACAGGAATGGGACTCGGCTGGTGGTGGAGAAAGAACATCCTCAGCTAGGG 442
Qy 136 AlaGlyThrValLeuLeuAlaGlyPheTyrAlaValSerPheLeuSerValAla 155
Db 441 GCTGGTACAGTCTCTCTCTCGGGCTGGATTCTATGCTGTGACGTTTCTCTCTGTGGCC 382
Qy 156 ValGlySerThrValTyrGlnGlyLys-Cys----- 166
Db 381 GTGGGACGACCGCTATTATACAGGGCAAAATATGCCAAATCTACTCTCTCCGGATTCCCC 322
Qy 167 -----LeuThrTyrLysGlyProArgArgGlnLeuPr 177
Db 321 CAATCTGAATTTTCCCTTCCACCAGGCTCTACCTCTGGAAAGGTCCAGAGGCGAGCTGCC 262
Qy 177 oAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProPr 197
Db 261 GGCCTGGTCCAGGGCCCTCCACCACCATGTGGAGCTCAGCAGATCTGCTTCCCTCC 202
Qy 197 oValProGlyGly 201
Db 201 AGTCCAGGAGGC 189

RESULT 12

BG744382
LOCUS
DEFINITION 602723117F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849421 5',
809 bp mRNA linear EST 15-MAY-2001

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG744382
BG744382.1 GI:14055035
EST
Homo sapiens (human)
Homo sapiens

mRNA sequence.

BG744382
GI:14055035
EST
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 809)

NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L10CM1689 row: a column: 06

High quality sequence stop: 719.

Location/Qualifiers

1..809

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4849421"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_106"

/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,55e-56 Length: 809
Score: 706.50 Matches: 153
Percent Similarity: 91.2% Conservative: 3
Best Local Similarity: 89.5% Mismatches: 9
Query Match: 66.2% Indels: 6
DB: 2 Gaps: 1

US-10-696-259-6 (1-201) x BG744382 (1-809)

Qy

1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20

Db

230 ATGGCTGGATGCTGTGTCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCTGG 289

Qy

21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40

Db

290 GTGTCCAGGCCCTCGAGATTCGTACCTCGAAGGATCCTTGCTTCTTCCCTCGCTCC 349

Qy

41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60

Db

350 TTCATGCCAGCCAGGAGACTGGCCATTTGGCTTCCTGTCACGTGGTTCGAGATGAGGTG 409

Qy

61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80

Db

410 GTTCCAGGAGGAGGTGAGGATGGGACCCACAGATTCAGGGCCGCTGSCCCACTT 469

Qy

81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100

Db

470 GCTTCTTCCGCTTTCCTCCATGACACACAGGCTGAGCTGCACATCCGGGCGCGAGGC 529

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Qy 101 HisAspAlaSerIleTyr---ValCysArgValGluValLeuGlyLeuGlyValGlyThr 119
Dy 530 CATGACGCCAGCATCTACCGTGTGCACGAGTGGCAGGTGCTGGGCTTGGTGTGGGACC 589
Qy 120 -GlyAsnGlyThrArgLeuValValGlu-LysGluHisProGlnLeuGlyAlaGly-Thr 138
Dy 590 AGGGAATGGGACTCGGCTGGTGGTGCACGACCGAACCTCCTCAGCTACGCGCTGGCTACA 649
Qy 139 ValLeuLeuLeuArg-alaGlyPheTyrAlaValSerPheLeu-SerValAlaValGlyS 158
Dy 650 GTCTCTCTCTTCGGGGCTGCATTTATGTGTGTGAGCTTTCTTCTGTGGCCGTGGGCA 709
Qy 158 erThrValTyrGlnGlyLys 165
Dy 710 GCACCGTCTATCACCAGGCCCAA 732

RESULT 13
BG398004 602439532F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565983 5',
LOCUS mRNA sequence.
DEFINITION BG398004.1 GI:13291452
ACCESSION BG398004
VERSION BG398004.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI283 row: o column: 08
High quality sequence stop: 628.
FEATURES
Location/Qualifiers
source 1..637
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4565983"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCACAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

ORIGIN

Alignment Scores:
Pred. No.: 3.64e-51 Length: 637
Score: 653.00 Matches: 131
Percent Similarity: 97.1% Conservative: 1
Best Local Similarity: 96.3% Mismatches: 3
Query Match: 61.2% Indels: 2
DB: 2 Gaps: 0

US-10-696-259-6 (1-201) x BG398004 (1-637)

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Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Dy 230 ATGCGCTGGATGCTGTGTGCTCTCTCTGATCATGTCTCCATCCAGATCCTGTGCTCTCTGG 289
Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Dy 290 GTGTCCCGAGCCCTGAGATTCTGACCTGGAAGGATCCTCTGCCTTCCTGCCCTGCTCC 349
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Dy 350 TTCAATCCAGCCCAAGGAGACGTGGCCATTGGTCTCCGTCCACGTGTTCCGAGATGAGGTG 409
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Dy 410 GTTCCAGGAAG-GAGGTGAGGAATGGAAACCCAGAGTTACGGCCGCCCTGGCCCCACTG 468
Qy 81 -AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgG 100
Dy 469 TGCTTCTTCCCGTTTCTCTCATGACCACAGGCTGAGTCGCATCCGGGACGTCGCGAGG 528
Qy 100 yHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrG 120
Dy 529 CCATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTGCGGACAGG 588
Qy 120 yAsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGly 135
Dy 589 GAATGGGACTCGGCTGGTGTGGAGAAAGACCATCTCTCAGTAGGGG 634

RESULT 14
BM363549 574 bp mRNA linear EST 10-JAN-2002
LOCUS BS320057A20D02 Subtracted Lewin Cattle Spleen cDNA clone
DEFINITION BS320057A20D02 5', mRNA sequence.
ACCESSION BM363549
VERSION BM363549
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 574)
AUTHORS Lewin,H.A., Soares,M.B., Pardinaz,J., Liu,L. and Larson,J.H.
TITLE Subtracted Lewin Cattle Spleen ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for Cattle EST sequencing was provided by the USDA National
Research Initiative, Project No. 98-35205-6644, and a grant from
the Japanese Ministry of Agriculture Fisheries and Forestry to
H.A.Lewin and J.E.Womack. Base-calling/Quality scores: PHRED form
Washington University Genome Center. Vector-trimming: Cross Match
from Washington University Genome Center PHRAP suite. This sequence
is vector free and at least 200bp in length.
Insert Length: 574 Std Error: 0.00
Plate: BS320057A20 row: D column: 02
Seq primer: CGCCAGCTCGAAATTAAACC
High quality sequence stop: 574.
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Location/Qualifiers
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/mol_type="mRNA"
/strain="Angus"
/db_xref="taxon:9913"
/clone="BS320057A20D02"
/sex="female"
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/dev_stage="Adult"
/clone_lib="Subtracted Lewin Cattle Spleen"
/note="Organ: Spleen; Vector: pBluescript SK(+/-); Site 1:
ECORI; Site 2: XhoI; This BS cDNA library was generated by
subtraction of the original non-normalized bovine spleen
library with 16,800 previously sequenced clones from a
bovine placenta cDNA library. The original library was
constructed as described by Band et al (2000), Genome
Research 10(9): 1359-1368."

ORIGIN

Alignment Scores:
Pred. No.: 2.79e-50 Length: 574
Score: 643.00 Matches: 126
Percent Similarity: 85.0% Conservative: 10
Best Local Similarity: 78.8% Mismatches: 24
Query Match: 60.3% Indels: 0
DB: 3 Gaps: 0

US-10-696-259-6 (1-201) x BM363549 (1-574)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 93 ATGGCCAGATGCTGTTTATCATCTTTATCATCTCGTCCAGGATCTTGTTCTCTGG 152
Qy 21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 153 GTGTCCAGGCCCTGAAATCCGTACCCAGGAGGGTCCCGGCTTCTGCTGTTCC 212
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 213 TTCATGCCACCAAGGAGTTTGCCCAATGGTCTGTGTCACATGGTACCGGACAAAGTG 272
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 273 GCCCAGGATGGAGGTGAGGAATGAGACCCAGAGTTCAGGCGCGCTGGCCCTCTC 332
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 333 CCTCTTCCCGCTTCTCTGTGACCCAGGCTGAGTGCACATCTGGGACACCGAGGC 392
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 393 CGTGACACTGGAGTCACTGCTGAGGTGAGGTGAGTGTGGGCTGGGTCGGAACAGG 452
Qy 121 AsnGlyThrArgLeuValValGlyLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 453 AATGGGACCTGCTGGTGGTGGAGGAGGAGCTCTCAGCTAGCGGCTGGCACAGTCTTC 512
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 513 CTCCTCGGGCTGGATCTATGCCTTCAGCTTCTCTCGGTGGCTATGGGCAGCAGCATG 572

RESULT 15

AW967444 719 bp mRNA linear EST 01-JUN-2000
LOCUS
DEFINITION EST379519 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
ACCESSION AW967444

VERSION AW967444.1 GI:8157281

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 719)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,

Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and

Quackenbush, J.

Assessment of gene expression patterns in a model of colon tumor

metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

Contact: John Quackenbush

COMMENT

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 241

Seq primer: Forward.

Location/Qualifiers

source

1. 719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGJ"
/note="vector: pBluescriptSKm"

ORIGIN

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Percent Similarity: 87.0% Conservative: 3
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Query Match: 58.1% Indels: 1
DB: 1 Gaps: 0

US-10-696-259-6 (1-201) x AW967444 (1-719)

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Qy 21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 344 GTGTCCAGGCCCTGAGAAATCGTACCTCGAAAGGATCTCTGCTTCTGCTGCTGCTCC 403
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 404 TTCATGCCACCAAGGAGTGGCCATTTGGCTTCCTGTCACGTGTTCCGAGATGAGGG 463
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 464 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTCAGGGGCGCTGGCCCATCTT 523
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 524 GCTTCTTCCCGTTCCTCCATGACCAACAGCTGAGCTGGACATTCGGGACGTGCGAGGC 583
Qy 101 HisAspAlaSerIleTyrValCys-ArgValGluValLeuGlyLeuGlyThrGly 120
Db 584 CATGACCCAGCATTTACCTGTGCAAGAGTGGAGGGGCTTGGCCCTGGGGTCGGGACAGG 643
Qy 120 YAsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLe 140
Db 644 GAATGGGAATTCGTTGTGGGGGGAAGAACAACCTCACTAGGGGCTGGTTCAAGACT 703
Qy 140 uLeuLeuArgAlaGly 145
Db 704 TCCCGCTGCGGTGGA 719

Search completed: February 28, 2006, 10:13:48

Job time : 3882 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 06:56:54 ; Search time 192 Seconds
(without alignments)
1860.885 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAWMLLILILVHPGSCALW.....APLPPPCGSSAHLPPVPG 201

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delep 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	126.5	11.9	8100	3	US-09-949-016-13460
3	126.5	11.9	8100	3	US-09-949-016-13461
4	120	11.2	1108	3	US-09-949-016-1718
5	120	11.2	1108	3	US-09-949-016-1719
6	118.5	11.1	1313	3	US-09-949-016-5578
7	116.5	10.9	672	3	US-09-023-655-1242
8	116.5	10.9	672	3	US-09-949-016-731
9	116	10.9	700	3	US-09-311-784A-31

c 10	115	10.8	669	3	US-09-646-561-44	Sequence 44, Appl
11	115	10.8	669	3	US-09-646-561-45	Sequence 45, Appl
12	115	10.8	1856	3	US-09-646-561-41	Sequence 41, Appl
c 13	115	10.8	1856	3	US-09-646-561-43	Sequence 43, Appl
14	113.5	10.6	2220	3	US-10-104-047-1739	Sequence 1739, Ap
15	112	10.5	669	3	US-09-646-561-49	Sequence 49, Appl
c 16	112	10.5	669	3	US-09-646-561-50	Sequence 50, Appl
17	112	10.5	1883	3	US-09-646-561-46	Sequence 46, Appl
c 18	112	10.5	1883	3	US-09-646-561-48	Sequence 48, Appl
19	110.5	10.4	804	2	US-08-416-336-1	Sequence 1, Appli
20	110.5	10.4	2418	3	US-09-949-016-1694	Sequence 1694, Ap
21	110	10.3	561	2	US-08-067-884-13	Sequence 13, Appl
22	110	10.3	561	2	US-08-008-898-13	Sequence 13, Appl
23	110	10.3	561	2	US-08-459-818-13	Sequence 13, Appl
24	110	10.3	561	2	US-08-889-666-13	Sequence 13, Appl
25	110	10.3	561	2	US-08-765-078-13	Sequence 13, Appl
26	110	10.3	561	2	US-08-725-776-13	Sequence 13, Appl
27	110	10.3	561	2	US-08-488-062-13	Sequence 13, Appl
28	110	10.3	561	3	US-08-228-208A-13	Sequence 13, Appl
29	110	10.3	561	3	US-08-253-783-35	Sequence 35, Appl
30	110	10.3	561	3	US-09-454-651B-13	Sequence 13, Appl
31	110	10.3	561	6	PCT-US95-06726-35	Sequence 35, Appl
32	109	10.2	749	3	US-09-303-040-9	Sequence 9, Appli
33	109	10.2	805	3	US-09-620-312D-62	Sequence 62, Appl
34	109	10.2	938	3	US-09-828-995B-25	Sequence 25, Appl
c 35	109	10.2	938	3	US-09-828-995B-27	Sequence 27, Appl
36	109	10.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
37	109	10.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
38	108.5	10.2	1985	3	US-09-907-794A-212	Sequence 212, App
39	108.5	10.2	1985	3	US-09-905-125A-212	Sequence 212, App
40	108.5	10.2	1985	3	US-09-902-775A-212	Sequence 212, App
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42	108.5	10.2	1985	3	US-09-903-603A-212	Sequence 212, App
43	108.5	10.2	1985	3	US-09-904-920A-212	Sequence 212, App
44	108.5	10.2	1985	3	US-09-909-064-212	Sequence 212, App
45	108.5	10.2	1985	3	US-09-905-381A-212	Sequence 212, App

ALIGNMENTS

RESULT 1
US-08-973-544-1/c
; Sequence 1, Application US/08973544
; Patent No. 6338950
; GENERAL INFORMATION:
; APPLICANT: WEISS, Elisabeth
; TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAITO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,544
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT EP 96/02663
; FILING DATE: 20-JUN-1996
; PRIOR APPLICATION DATA: EP 95109511.6
; APPLICATION NUMBER: EP 95109511.6
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112201.9
; FILING DATE: 03-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Kitts, Monica Chin
 REGISTRATION NUMBER: 36,105
 REFERENCE/DOCKET NUMBER: P8341-7073
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5000
 TELEFAX: (202) 638-4810

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5581 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:

NAME/KEY: exon

LOCATION: 48..162

FEATURE:

NAME/KEY: exon

LOCATION: 544..652

FEATURE:

NAME/KEY: exon

LOCATION: 1044..1162

FEATURE:

NAME/KEY: exon

LOCATION: 1475..1567

FEATURE:

NAME/KEY: exon

LOCATION: 1775..1797

FEATURE:

NAME/KEY: exon

LOCATION: 2325..2709

FEATURE:

US-08-973-544-1

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Pred. No.: 1.27e-71 Length: 5581
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US-10-696-259-6 (1-201) x US-08-973-544-1 (1-5581)

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 Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
 Db 3888 TTCTGTCCCTGCTCTTCAATGCCAGCCCAAGGAGACTGGCATTTGGCTCCGTCACTGG 3829
 Qy 56 PheArgAspGluValValProGluGlyGluValArgAsnGlyThrProGluPheArgGly 75
 Db 3828 TTCCGAGATGAGGTGTTCCAGGAAGAGGTGAGGAATGAACCCAGAGATTCCAGGGGC 3769
 Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
 Db 3768 CGCCT----CCATCTGCTTCTTCCGGTTCTCTCATGTAGACACCCAGGCTGAGCTGCACATC 3713
 Qy 96 ArgAspValArgGlyHisAspAla-SerIleTrpValCysArgValGluValLeuGlyLe 115
 Db 3712 CGGACGTGCCAGGCCATGACCCAGGCATTTACGTGTGCAGATGGAGGTGTGGGCTT 3653
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 Db 3652 TGGTGTCCGGACAGGAATGGACTCGCTGGTGTGGAGAAAGTGAGATGCTGGGAGG 3593
 Qy 129 ----- 129
 Db 3592 TGGTGTCTCTCCTGGTGGAGGCCAAGAGGCAATGTCTTTGGAGGACGAGATGTCTCC 3533
 Qy 129 ----- 129

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 Db 3413 TCTATGCTGTCACTTCTCTGTGGCGTGGGACGACCGTCTATTACAGGGCAAT 3354
 Qy 166 ys----- 166
 Db 3353 GTGAGTAATGGACGGGCAATAGTGGACGGATGGGAGGGGAGTAAGAGAGTGGGA 3294
 Qy 166 ----- 166
 Db 3293 GGAGGGAGGACAGAGACCAGGAAGAGAGAGCCCTCGGACTGCAACACTGAGCAGTCTC 3234
 Qy 166 ----- 166
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 Qy 166 ----- 166
 Db 3113 TGCCCCACCACTAACTCTCATGAGTCTCAAGTGTCTTCTTCTCATTCTCCAGATGCCA 3054
 Qy 167 -----LeuThrTrp 169
 Db 3053 AATCTACTCTCTCGGATTCCTCCCACTCTGAACCTTCCCTTCCACGAGTCTGACCTGG 2994
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 Db 2993 AAAGTCCAAAGAGGACGCTGCCGCTGTGTCAGCGCCCTCCACCATCATGTGGG 2934
 Qy 190 SerSerAlaHisLeuLeuProProValProGlyGly 201
 Db 2933 AGCTCAGCACATCTGCTTCTCCCGAGTCCAGGAGGC 2898

RESULT 2

US-09-949-016-13460
 ; Sequence 13460, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CU001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13460
 ; LENGTH: 8100
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-13460

Alignment Scores: 0.0129 Length: 8100
 Pred. No.: 126.50 Matches: 64
 Percent Similarity: 38.9% Conservatives: 20
 Best Local Similarity: 29.6% Mismatches: 82


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Query Match: 11.9% Indels: 50
DB: 3 Gaps: 12

US-10-696-259-6 (1-201) x US-09-949-016-13460 (1-8100)

Qy 14 ProGlySerCysAlaLeuTrpValSerGln---ProProGluLeuLeuArgThrLeuGluGly 32
Db 3724 CCTGGGTGCAGCCCTGTGGATGCAAGGTCCACAGTCATCATGTGGTGAGCGCTGGGG 3783

Qy 33 SerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySer 52
Db 3784 GAAGAGCCCATCTCCATGTCCTCCACATAGCAGCAACAC-----GCCAAC 3831

Qy 53 ValThrTrpPheArgAspGluValValProGlyLysGluValArgAsnGlyThr----- 70
Db 3832 GTCACTGGTGGCGC-----GTCTCCATGGC-----AACTACACGTGGGCC 3873

Qy 71 ProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGln 90
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Qy 91 AlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArgVal 110
Db 3907 GGTACGCTGATCATCCAGATGTGAACAGAGCCATGGGGCATATACGTGTGCCGGGTC 3966

Qy 111 GluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGlu 130
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Qy 142 -----LeuArgAlaGlyPheTyr-----AlaValSe 150
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Qy 150 rPheLeuSerValAlaValGlySerThrValTyrGlnGlyLysCysLeuThrTrpLy 170
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Qy 170 sGlyPro-----ArgArgGlnLeuProAlaValValProAlaProLeuProPr 186
Db 4204 GGGGCCAGAGGCTAGGAGGCAAGAGGGGCCAGGCTC-----TGAGCCATACTACC 4257

Qy 186 oProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 4258 TCCTTGAGAGCGCCCGCCCGCCCGCCCTTCTTGACATGGGGAGGG 4303

RESULT 3
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; Sequence 13461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13461
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13461
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Alignment Scores:
Pred. No.: 0.0129 Length: 8100
Score: 126.50 Matches: 64
Percent Similarity: 38.9% Conservative: 20
Best Local Similarity: 29.6% Mismatches: 82
Query Match: 11.9% Indels: 50
DB: 3 Gaps: 12

US-10-696-259-6 (1-201) x US-09-949-016-13461 (1-8100)

Qy 14 ProGlySerCysAlaLeuTrpValSerGln---ProProGluLeuLeuArgThrLeuGluGly 32
Db 3724 CCTGGGTGCAGCCCTGTGGATGCAAGGTCCACAGTCATCATGTGGTGAGCGCTGGGG 3783

Qy 33 SerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySer 52
Db 3784 GAAGAGCCCATCTCCATGTCCTCCACATAGCAGCAACAC-----GCCAAC 3831

Qy 53 ValThrTrpPheArgAspGluValValProGlyLysGluValArgAsnGlyThr----- 70
Db 3832 GTCACTGGTGGCGC-----GTCTCCATGGC-----AACTACACGTGGGCC 3873

Qy 71 ProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGln 90
Db 3874 CCTGAGTCTTGGGCCCG-----GGCGAGGACCCCAAT 3906

Qy 91 AlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArgVal 110
Db 3907 GGTACGCTGATCATCCAGATGTGAACAGAGCCATGGGGCATATACGTGTGCCGGGTC 3966

Qy 111 GluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGlu 130
Db 3967 CAGGAGGGCAACAGTATACAGAGTCCTCGCGCACCTACCTCCCGTGGCGCGTGAG 4026

Qy 131 HisProGlnLeuGly-----Ala-GlyThrValLeuLeu----- 141
Db 4027 TGGCCAGCCCTGGCCCTACTCCACTGTCCTGGGACACTCGGTTTATCTTTGAA 4086

Qy 142 -----LeuArgAlaGlyPheTyr-----AlaValSe 150
Db 4087 GTGGGATAGAGCCAGTACCTTCATGTGGTTCAACCGGCTTGACAGAGGACGGA 4146

Qy 150 rPheLeuSerValAlaValGlySerThrValTyrGlnGlyLysCysLeuThrTrpLy 170
Db 4147 CATCTCTCTGCAGAGTGGGGTCT---CTGGGGGTCTGGGGCTTGCAGGAGTGGGC 4203

Qy 170 sGlyPro-----ArgArgGlnLeuProAlaValValProAlaProLeuProPr 186
Db 4204 GGGGCCAGAGGCTAGGAGGCAAGAGGGGCCAGGCTC-----TGAGCCATACTACC 4257

Qy 186 oProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 4258 TCCTTGAGAGCGCCCGCCCGCCCGCCCTTCTTGACATGGGGAGGG 4303

RESULT 4
US-09-949-016-1718
; Sequence 1718, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13461
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1718
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Best Local Similarity: 27.0% Mismatches: 93
 Query Match: 10.9% Indels: 29
 DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-023-655-1242 (1-672)

QY 6 LeuLeuLeuLeuLeuMetValHisProGlySerCys---AlaLeuTrpValSerGlnPro 24
 Db 70 CTCCTGTTTTCTCTCTCTCATCCCTGCTCTTCTGAAAGCAATGACAGTGGCCAGCCT 129
 QY 25 ProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSer 44
 Db 130 GCTGTGTACTGCGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTAT---GCACT 186
 QY 45 GlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValProGlyLys 64
 Db 187 CAGGCAAGCCACTGAGTCCGGGTGACAGTCTTCGGCAGGCTGACAGCCAGGTGACT 246
 QY 65 GluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArg 84
 Db 247 GAAGTCTGTGCGCAACCTACATGACGGGAATGAGTTGACC----- 288
 QY 85 PheLeuHisAsp-----HisGlnAlaGluLeuHisIle 95
 Db 289 TTCCTAGATGATTCCTATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATC 348
 QY 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu----- 113
 Db 349 CAAGGACTGAGGCCATGACAGCGGACTCTACATCTGCAAGGTGGAGCTCATGTACCA 408
 QY 114 ---GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValGluLysGluHisPro 132
 Db 409 CGCCATACCTAGTGGCATAGCAACGCAACCCAGATTATGTAATTGATCCAGAACCG 468
 QY 133 GlnLeuGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAla 148
 Db 469 TGCCAGATCTGAGTCTCTCTCGATCTTCGACGAGTGTAGTTCGGGGTGTGTTTTT 528
 QY 149 ValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThr 168
 Db 529 TATAGCTTCTCTCACAGCTGTTCTTTGAGC-----AAATGCTAAAG 573
 QY 169 TrpLysGlyProArgArgGlnLeuProAlaValProAlaProLeuProProCys 188
 Db 574 AAAAGAAGCCCTTTACACAGGGGTCTATGTGAAATGCCCCCAACAGACCGAGAATGT 633

RESULT 8

US-09-949-016-731
 ; Sequence 731, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 731
 ; LENGTH: 672
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-731

Alignment Scores:
 Pred. No.: 0.00404 Length: 672

Score: 116.50 Matches: 54
 Percent Similarity: 39.0% Conservative: 24
 Best Local Similarity: 27.0% Mismatches: 93
 Query Match: 10.9% Indels: 29
 DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-949-016-731 (1-672)

QY 6 LeuLeuLeuLeuLeuMetValHisProGlySerCys---AlaLeuTrpValSerGlnPro 24
 Db 70 CTCCTGTTTTCTCTCTCTCATCCCTGCTCTTCTGAAAGCAATGACAGTGGCCAGCCT 129
 QY 25 ProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSer 44
 Db 130 GCTGTGTACTGCGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTAT---GCACT 186
 QY 45 GlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValProGlyLys 64
 Db 187 CAGGCAAGCCACTGAGTCCGGGTGACAGTCTTCGGCAGGCTGACAGCCAGGTGACT 246
 QY 65 GluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArg 84
 Db 247 GAAGTCTGTGCGCAACCTACATGACGGGAATGAGTTGACC----- 288
 QY 85 PheLeuHisAsp-----HisGlnAlaGluLeuHisIle 95
 Db 289 TTCCTAGATGATTCCTATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATC 348
 QY 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu----- 113
 Db 349 CAAGGACTGAGGCCATGACAGCGGACTCTACATCTGCAAGGTGGAGCTCATGTACCA 408
 QY 114 ---GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValGluLysGluHisPro 132
 Db 409 CGCCATACCTAGTGGCATAGCAACGCAACCCAGATTATGTAATTGATCCAGAACCG 468
 QY 133 GlnLeuGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAla 148
 Db 469 TGCCAGATCTGAGTCTCTCTCGATCTTCGACGAGTGTAGTTCGGGGTGTGTTTTT 528
 QY 149 ValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThr 168
 Db 529 TATAGCTTCTCTCACAGCTGTTCTTTGAGC-----AAATGCTAAAG 573
 QY 169 TrpLysGlyProArgArgGlnLeuProAlaValProAlaProLeuProProCys 188
 Db 574 AAAAGAAGCCCTTTACACAGGGGTCTATGTGAAATGCCCCCAACAGACCGAGAATGT 633

RESULT 9

US-09-311-784A-31
 ; Sequence 31, Application US/09311784A
 ; Patent No. 6534482
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.01
 ; CURRENT APPLICATION NUMBER: US/09/311,784A
 ; CURRENT FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,751
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 700
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens


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; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-646-561-45

Alignment Scores:
Pred. No.: 0.00579 Length: 669
Score: 115.00 Matches: 53
Percent Similarity: 42.7% Conservative: 32
Best Local Similarity: 26.6% Mismatches: 97
Query Match: 10.8% Indels: 28
DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-646-561-45 (1-669)

QY 6 LeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro 25
Db 597 CTGTTTCTCTCTCTTTATCCCGCTCTTCCAAAGGATGCATGGCTCAGCCTGCA 538

QY 26 GluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPhe----- 41
Db 537 GTGGTCTCGCCAGCAGCGGGGTGTTCTAGCTTCGTGTGTAATATGGTCTTCAGGC 478

QY 42 AsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 61
Db 477 AACGACGCGAGGTCCGGGTGCAGTGTCT-CCGCGAGGCTGGCAGCCAGATGACTGA 419

QY 62 ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAla 81
Db 418 CTGTGCCCGACATACACAGTGA-----GGATGAGTGGC---CTTCCT 377

QY 82 SerSerArgPheLeuHisAspHis-----GlnAlaGluLeuHisIleArgAsp 97
Db 376 GGATGATTCTACCTGCACCGGCACCTCCAGTGGAAACAAAGTGAACCTCACCATCCA 317

QY 98 ValArgGlyHis-AspAlaSerIleTyrValCysArgValGluValLeu----- 114
Db 316 GTTAGGCGCCATGACACGCGGGCTCTACATCTCAAGGTGGAGTCTATGTACCCACC 257

QY 114 YLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGlnLe 134
Db 256 CTACTATGTAGCATGGAAATGAAACCCAGATTATGTCTATCGATCTGAACTTGCCC 197

QY 134 uGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaValSe 150
Db 196 AGATTCTGACTTCCTCTCTCGATCTTCAGCAGTCAGTTCGGGCTTGTTTTTTATAG 137

QY 150 rPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrpLy 170
Db 136 CTTTCTTATCACAGCTGTTCTTTGAGC-----AAATGCTAAAGAAAG 92

QY 170 sGlyProArgGlnLeuProAlaValValProAlaProLeuProProCys 188
Db 91 AAGCCCTCTTACCACAGGGGTCTATGTGAAATGCCCCCACTGAGCCAGAAATGT 37

RESULT 12
US-09-646-561-41
; Sequence 41, Application US/09646561
; Patent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IN-1-C1-PCT
; CURRENT APPLICATION NUMBER: US/09/646,561
; CURRENT FILING DATE: 2000-09-19

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; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 1856
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (60)..(731)
US-09-646-561-41

Alignment Scores:
Pred. No.: 0.0255 Length: 1856
Score: 115.00 Matches: 53
Percent Similarity: 42.7% Conservative: 32
Best Local Similarity: 26.6% Mismatches: 87
Query Match: 10.8% Indels: 28
DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-646-561-41 (1-1856)

QY 6 LeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro 25
Db 132 CTGTTTCTCTCTCTTTATCCCGCTCTTCCAAAGGATGCATGGCTCAGCCTGCA 191

QY 26 GluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPhe----- 41
Db 192 GTGGTCTCGCCAGCAGCGGGGTGTTCTAGCTTCGTGTGTAATATGGTCTTCAGGC 251

QY 42 AsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 61
Db 252 AACGACGCGAGGTCCGGGTGCAGTGTCT-CCGCGAGGCTGGCAGCCAGATGACTGA 310

QY 62 ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAla 81
Db 311 CTGTGCCCGACATACACAGTGA-----GGATGAGTGGC---CTTCCT 352

QY 82 SerSerArgPheLeuHisAspHis-----GlnAlaGluLeuHisIleArgAsp 97
Db 353 GGATGATTCTACCTGCACCGGCACCTCCAGTGGAAACAAAGTGAACCTCACCATCCA 412

QY 98 ValArgGlyHis-AspAlaSerIleTyrValCysArgValGluValLeu----- 114
Db 413 GTTAGGCGCCATGACACGCGGGCTCTACATCTCAAGGTGGAGTCTATGTACCCACC 472

QY 114 YLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGlnLe 134
Db 473 CTACTATGTAGCATGGAAATGAAACCCAGATTATGTCTGATCTCGTGAACCTTGCCC 532

QY 134 uGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaValSe 150
Db 533 AGATTCTGACTTCCTCTCTCGATCTTCAGCAGTCAGTTCGGGCTTGTTTTTTATAG 592

QY 150 rPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrpLy 170
Db 593 CTTTCTTATCACAGCTGTTCTTTGAGC-----AAATGCTAAAGAAAG 637

QY 170 sGlyProArgGlnLeuProAlaValValProAlaProLeuProProCys 188
Db 638 AAGCCCTCTTACCACAGGGGTCTATGTGAAATGCCCCCACTGAGCCAGAAATGT 692

RESULT 13
US-09-646-561-43/c
; Sequence 43, Application US/09646561
; Patent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.

```

```
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES, AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/646,561
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 1856
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-646-561-43

Alignment Scores:
Pred. No.: 0.0255 Length: 1856
Score: 115.00 Matches: 53
Percent Similarity: 42.7% Conservative: 32
Best Local Similarity: 26.6% Mismatches: 87
Query Match: 10.8% Indels: 28
DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-646-561-43 (1-1856)

Qy 6 LeuLeuIleLeuIleMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro 25
Db 1725 CTGTTTCTCTCTCTTATCCCCGCTTCTTCAAAGGAGTGCATGGCTCAGCCTGCA 1666

Qy 26 GluIleAArgThrLeuGluGlySerSerAlaPheLeuProCysSerPhe----- 41
Db 1665 GTGGTTCTGGCCAGCAGCGGGGTGTGCTAGCTTGTGTGTAATATGGTCTTTCAGGC 1606

Qy 42 AsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValVal 61
Db 1605 AACACACCCGAGTGGCGGTGCACAGTGTCT-GCGGACGGCTGGCAGCCAGATGACTGAAGT 1547

Qy 62 ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAla 81
Db 1546 CTGTGCGCGGACATACACAGTGGG-----GGATGAGTTGGC---CTTCCT 1505

Qy 82 SerSerArgPheLeuHisAspHis-----GlnAlaGluLeuHisIleArgAsp 97
Db 1504 GGATGATTCTACCTGCACCGGCACCTCCAGTGGAAACAAAGTGAACCTCACCTCCAAGG 1445

Qy 98 ValArgGlyHis-AspAlaSerIleTyrValCysArgValGluValLeu-----G1 114
Db 1444 GTTGAGGGCCATGCACACGGGGCTCTACATCTGCAAGGTGGAGCTCATGTACCCACCACC 1385

Qy 114 YLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGlnLe 134
Db 1384 CTACTATGTAGGCATGGAAATGAAACCCAGATTATGTATCATGCATCCTGAACCTGCC 1325

Qy 134 uGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaValSe 150
Db 1324 AGATTCTGACTTCTCTCTGATCCTTGACAGCAGTCAGTTCGGGCTGTTTTTTATAG 1265

Qy 150 rPheLeuSerValAlaValGlySerThrValTyr-Tyr-GlnGlyLysCysLeuThrTrpLy 170
Db 1264 CTTTCTTATCACAGCTGTTCTTTGAGC-----AAAAATGCTAAAGAAAAG 1220

Qy 170 sGlyProArgGlnLeuProAlaValValProAlaProLeuProProProCys 188
Db 1219 AAGCCCTCTTACCACAGGGGTCTATGTGAAATAATCCCCCACTGAGCCAGAATGT 1165

RESULT 14
US-10-104-047-1739
; Sequence 1739, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE.
```

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; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1739
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1739

Alignment Scores:
Pred. No.: 0.0477 Length: 2220
Score: 113.50 Matches: 50
Percent Similarity: 37.4% Conservative: 18
Best Local Similarity: 27.5% Mismatches: 72
Query Match: 10.6% Indels: 42
DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-10-104-047-1739 (1-2220)

Qy 15 GlySerCysAlaLeuTrpValSerGlnPro-----ProGluIle 27
Db 707 GGGGAAGACGGCGGTGGTGGTCAAGTCCACCAGTGCAGAAATGGCCTCCACAGACCTG 766

Qy 28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg 47
Db 767 TCCACCACCAAGGCTCCACGCTTCTTGCTTGAAGCGGAGGCGAGTCTCTAG--- 823

Qy 48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg 67
Db 824 -----CCCAACATCACCTGGGACAAAGAT----- 847

Qy 68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis 87
Db 848 -----GGCCAGCTGTGTGGGCGCCGAGGGGAAAGTTCCACCATC 886

Qy 88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrVal 107
Db 887 CAGCCTTCTGGGAGTGTGTGTGAAGAACTTGGAGGGCCAGGACGACCTATACC 946

Qy 108 CysArgValGlu---ValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuVal 126
Db 947 TGTAACCGCTGAGAACCGCGTGGGCGCGCGCGCGCGGTGCACCTCACCATCTCTGGTA 1006

Qy 127 ValGluLys-GluHisProGlnLeuGly---AlaGlyThrValLeuLeuLeuArgAlaG1 145
Db 1007 CTGCTGTGTTCACCACCTGCTGGGGACCGCAGCTGCGCTTGGGGACAGGCTGTGG 1066

Qy 145 yPhe-----TyrAlaValSerPheLeuSerValAlaVal 156
Db 1067 CTTGCTGTGTCAGCCCGGGGACGCCACCCCTCGCATTCGCTGGAATGTGTCACACGACCG 1126

Qy 156 lGlySerThrValTyr-Tyr-GlnGlyLysCysValLeuThrTrpLysGlyProArgGlnLe 176
Db 1127 CCAGTCACAGTCTGGGTC-----TCTGGGATGGTGGGACAGAGCCAGGAC 1177

Qy 176 uPro 177
Db 1178 ACCG 1181

RESULT 15
US-09-646-561-49
; Sequence 49, Application US/09646561
; Patent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
```

/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

/ FILE REFERENCE: IM-1-CI-PCT

/ CURRENT APPLICATION NUMBER: US/09/646,561

/ CURRENT FILING DATE: 2000-09-19

/ PRIOR APPLICATION NUMBER: 60/078,765

/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 09/062,597

/ PRIOR FILING DATE: 1998-04-17

/ NUMBER OF SEQ ID NOS: 65

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 49

/ LENGTH: 669

/ TYPE: DNA

/ ORGANISM: Felis catus

/ US-09-646-561-49

Alignment Scores:

Pred. No.:	0.0121	Length:	669
Score:	112.00	Matches:	52
Percent Similarity:	38.2%	Conservative:	24
Best Local Similarity:	26.1%	Mismatches:	95
Query Match:	10.5%	Indels:	28
DB:	3	Gaps:	6

US-10-696-259-6 (1-201) x US-09-646-561-49 (1-669)

QY	6	LeuLeuIleLeuIleMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro	25
DB	73	CTGTTTTCTCTCTCTTTATCCCCCTCTTCCAAAGGATGTCATGTGGCCACGCTGCA	132
QY	26	GluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGln	45
DB	133	GTGGTGTGGCCAGCAGCGAGGTGTCGCCAGCTCGTGTGTAATATGGGTCTTCA---	189
QY	46	GlyArgLeuAlaIleGlySerValThrTrpPheArgaspGluValValProGlyLysGlu	65
DB	190	GGCAATGCCGCCGAAGTCCGAGTACTGTGTGAGGCAGACTGGCCAGCCAGATGACTGAA	249
QY	66	ValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPhe	85
DB	250	GTCTGTGTGGCAGATACACAGTGGAGATGAGTTGGCC-----TTC	291
QY	86	LeuHisAsp-----HisGlnAlaGluLeuHisIleArg	96
DB	292	CTAGATGATTCACCTGTCACCTGGCATCTCCAGCGGAAACAAAGTGAACCTCACCATCAA	351
QY	97	AspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu-----	113
DB	352	GGGTTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGGAGCTCATGTACCCACA	411
QY	114	GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGln	133
DB	412	CCCTACTATGCGGCATGGGCAATGGAACCCAGATTATGTATCATCGATCCTGAACTTGC	471
QY	134	LeuGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaVal	149
DB	472	CCAGATCTGACTTCTCTCTCTGATCTCGCAGCAGTCAAGTTCAGGATTGTTTTTTAT	531
QY	150	SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTip	169
DB	532	AGCTTCTTATACAGCTGTTCTTTGAGC-----AAATGCTAAAGAAA	576
QY	170	LysGlyProArgArgGlnLeuProAlaValProAlaProLeuProProProCys	188
DB	577	AGAAGCCCTCTTACTACAGGGGTCTATGTGAAATGCCCCAACAGAGCCAGATGT	633

Search completed: February 28, 2006, 07:19:18

Job time : 203 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 07:04:48 ; Search time 775 Seconds
(without alignments)
2144.703 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAMLLILILVHFGSCALW.....APLPPCGSSAHLPLPVPFG 201

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB_spool/US10696259/runat_27022006_123601_27279/app_query.fasta_1
-DB=Published Applications_NA_Main -QMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes03h
-USER=US10696259 @CGN 1 1 1026 @runat_27022006_123601_27279 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1067	100.0	1061	9	US-10-895-225A-31
2	1039	97.4	834	7	US-10-696-259-3
3	997	93.4	889	7	US-10-696-259-2
4	876	82.1	573	5	US-10-036-444-13
5	876	82.1	573	10	US-11-137-649-13
6	876	82.1	606	5	US-10-036-444-12
7	876	82.1	606	10	US-11-137-649-12

8	876	82.1	674	5	US-10-036-444-1	Sequence 1, Appli
9	876	82.1	674	10	US-11-137-649-1	Sequence 1, Appli
10	872	81.7	22173	7	US-10-322-696-28	Sequence 28, Appl
11	848	79.5	671	7	US-10-696-259-1	Sequence 1, Appli
12	773	72.4	5581	2	US-08-973-544-1	Sequence 10, Appl
13	728	68.2	421	5	US-10-036-444-10	Sequence 10, Appl
14	728	68.2	421	10	US-11-137-649-10	Sequence 10, Appl
15	713	66.8	405	7	US-10-333-481-15	Sequence 15, Appl
16	713	66.8	1110	7	US-10-333-481-16	Sequence 16, Appl
17	464.5	43.5	3673778	6	US-10-312-841-1	Sequence 1, Appli
18	440	41.2	3673778	6	US-10-312-841-2	Sequence 2, Appli
19	225.5	21.1	21781	7	US-10-322-696-25	Sequence 25, Appl
20	131.5	12.3	967	5	US-10-158-646-74	Sequence 74, Appl
21	126.5	11.9	44075	3	US-09-997-722-40	Sequence 40, Appl
22	125.5	11.8	869	3	US-09-909-567B-13	Sequence 13, Appl
23	125	11.7	636	3	US-09-898-195A-16	Sequence 16, Appl
24	125	11.7	636	5	US-10-057-288-11	Sequence 11, Appl
25	125	11.7	636	5	US-10-155-514-1	Sequence 1, Appli
26	125	11.7	636	7	US-10-419-008-16	Sequence 16, Appl
27	125	11.7	636	8	US-10-742-564A-5	Sequence 5, Appli
28	125	11.7	636	9	US-10-740-645A-5	Sequence 5, Appli
29	125	11.7	636	9	US-10-910-531-16	Sequence 16, Appl
30	125	11.7	11265	5	US-10-185-318-1	Sequence 1, Appli
31	125	11.7	11265	5	US-10-185-799-1	Sequence 1, Appli
32	122	11.4	1483	5	US-10-161-572-25	Sequence 25, Appl
33	122	11.4	1530	3	US-09-766-511B-32	Sequence 32, Appl
34	122	11.4	1533	3	US-09-972-268-32	Sequence 32, Appl
35	122	11.4	1533	7	US-10-058-270A-53	Sequence 53, Appl
36	122	11.4	1558	5	US-10-161-572-24	Sequence 24, Appl
37	122	11.4	2642	5	US-10-161-572-23	Sequence 23, Appl
38	122	11.4	2680	6	US-10-295-027-65	Sequence 65, Appl
39	122	11.4	2680	6	US-10-173-999-75	Sequence 75, Appl
40	122	11.4	2680	7	US-10-188-832-178	Sequence 178, App
41	122	11.4	3389	7	US-10-422-571-14	Sequence 14, Appl
42	122	11.4	3389	7	US-10-422-571-111	Sequence 111, App
43	122	11.4	3389	7	US-10-422-571-113	Sequence 113, App
44	122	11.4	3401	7	US-10-422-571-16	Sequence 16, Appl
45	122	11.4	3401	7	US-10-422-571-117	Sequence 117, App

ALIGNMENTS

RESULT 1
US-10-895-225A-31
; Sequence 31, Application US/10895225A
; Publication No. US20050048587A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Snyder, Jessica
; APPLICANT: Bagley, Andria
; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
; TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: TUN-025
; CURRENT APPLICATION NUMBER: US/10/895,225A
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/488,502
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1061
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-895-225A-31

Alignment Scores:			
Pred. No.:	2.02e-115	Length:	1061
Score:	1067.00	Matches:	201
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0


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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-696-259-2

Alignment Scores:
Pred. No.:      2,889-107      Length:      889
Score:          997.00        Matches:     199
Percent Similarity: 90.5%    Conservative: 0
Best Local Similarity: 90.5% Mismatches:   2
Query Match:     93.4%       Indels:      20
DB:              7           Gaps:       1

US-10-696-259-6 (1-201) x US-10-696-259-2 (1-889)
Qy      1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuValHisProGlySerCysAlaLeuTrrp 20
Db      66 ATGGCTGGATGCTGTTCATCTTGATCATGGTCCATCCAGGATCTGTCTCTCGG 125

Qy      21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db      126 GTGTCCAGCCCCCTGAGATTCTGTACCTGGGAAGGATCTCTGCCTTCTCTGCCCTGCTCC 185

Qy      41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db      186 TTCAATGCCAGCCAGGAGACTGGCCATTTGGCTCGCTCACGTGGTTCCGAGATGAGGTG 245

Qy      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db      246 GTTCCAGGGAAGAGAGTGAAGATGGAACCCCAGAGATTTCAG-GGGCGCCTGGCCCCACTT 304

Qy      81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db      305 GCCTCTTCCGTTTCTCCATGACCACAGGCTGAGCTGCACATCCGGGACGTGGAGGC 364

Qy      101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db      365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGTCTGGGCTTGGTCTCGGGACAGGG 424

Qy      121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db      425 AATGGGACTCGGCTGGTGGTGAGAAAGAACAATCTCTCAGTAGGGGCTGGTACAGTCTCTC 484

Qy      141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db      485 CTCTTCGGGCTGGATTCTATGCTGTGCAGCTTCTCTGTGTGGCCGTGGGACACCGCTC 544

Qy      161 TyrrTyrrGlnGlyLys-Cys----- 166
Db      545 TATTACAGGGCAAAATATGCCAANTACTCTCTCCGGATTCCCCCAACTCTGAACCTTTC 604

Qy      167 -----LeuThrTriplysGlyProArgArgGlnLeuProAlaValProAl 182
Db      605 CCTTCCACCAGGCTCTACCTCTGGAAGGTCCTCAAGAGGACAGCTGCCGGCTGTGGTCCAGC 664

Qy      182 aProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db      665 GCCCTTCCACCACCATGTTGGAGCTCAGCACATCTGCTTCCCCCAGTCCCCAGGAGGC 722

RESULT 4
US-10-036-444-13
; Sequence 13, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; FILE REFERENCE: SEQ-FR-1060

CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human NK cell
US-10-036-444-13

Alignment Scores:
Pred. No.:      3,01e-93      Length:      573
Score:          876.00        Matches:     173
Percent Similarity: 90.2%    Conservative: 2
Best Local Similarity: 89.2% Mismatches:   7
Query Match:     82.1%       Indels:      12
DB:              5           Gaps:       2

US-10-696-259-6 (1-201) x US-10-036-444-13 (1-573)
Qy      1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuValHisProGlySerCysAlaLeuTrrp 20
Db      1 ATGGCCTGGATGCTGTTCATCTTGATCATGGTCCATCCAGGATCTGTGTCTCTCTCGG 60

Qy      21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db      61 GTGTCCAGCCCCCTGAGATTCTGAPACCTCGAAGGATCTCTGCCTTCTCTGCCCTGCTGCC 120

Qy      41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db      121 TTCATGCCAGCCAGGAGACTGGCCATTTGGCTCCGTACGTGTTCGAGATGAGGTG 180

Qy      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db      181 GTTCCAGGGAAGAGGTGAGGAATGGAACCCCAGAGTTCCAGGGGCGCCTGGCCCCACTT 240

Qy      81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db      241 GCCTCTTCCGCTTTCCTCCATGACCACAGGCTGAGCTGCACATCCGGGACGTGCGAGGC 300

Qy      101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db      301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGTCTGGGCTTGGTGTGGGACAGGG 360

Qy      121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db      361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCTCAGCTAGGGGCTGTGTACAGTCTCTC 420

Qy      141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db      421 CTCCTTCGGGCTGGATTCTATGTGTGCAGCTTCTCTCTGTGGCTGGGACGACCGTC 480

Qy      161 TyrrTyrrGlnGlyLys-----CysLeuThrTriplysGlyPro 172
Db      481 TATTACAGGGCAAAATGCCACTGTACATGGGAACACACTGCCACTCTCAGATGGGCC 540

Qy      173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db      541 CGA-----GGRGGTGATTCCAGAGCCCGACAGATGTCCC 570

RESULT 5
US-11-137-649-13
; Sequence 13, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "Novel triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; FILE REFERENCE: SEQ-FR-1060

```


Publication No. US20050221438A1
 GENERAL INFORMATION:
 APPLICANT: INNATE PHARMA S.A.S.
 TITLE OF INVENTION: "Novel triggering receptor involved in natural
 TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
 TITLE OF INVENTION: antibodies that identify the same"
 FILE REFERENCE: SEQ-PR-1060
 CURRENT APPLICATION NUMBER: US/11/137,649
 CURRENT FILING DATE: 2005-05-25
 PRIOR APPLICATION NUMBER: US/10/036,444
 PRIOR FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: 09/440,514
 PRIOR FILING DATE: 1999-11-15
 PRIOR APPLICATION NUMBER: 09/456,199
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 12
 LENGTH: 606
 TYPE: DNA
 ORGANISM: Human NK cell
 US-11-137-649-12

Alignment Scores:
 Pred. No.: 3,23e-93 Length: 606
 Score: 876.00 Matches: 173
 Percent Similarity: 90.2% Conservative: 2
 Best Local Similarity: 89.2% Mismatches: 7
 Query Match: 82.1% Indels: 12
 DB: 10 Gaps: 2

US-10-696-259-6 (1-201) x US-11-137-649-12 (1-606)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
 Db 8 ATGGCCCTGGATGCTGTGCTCATCTTGATCATGGTCCATCCAGGATCTGTGCTCTCGG 67
 Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
 Db 68 GTGTCCACAGCCCTGAGATTGCTACCTCGAAGGATCTCTGCTTCTGCTCCCTGCTCC 127
 Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 Db 128 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTCCGAGATCAGGTG 187
 Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
 Db 188 GTTCCAGGGAAGGAGGTGAGGAATGGAAACCCAGAGTTCCAGGGCCGCTGGCCCACTT 247
 Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 248 GCTTCTCCGTTTCTCCATGACCAACAGGCTGAGCTGCATCCGGGAGCTGGAGGC 307
 Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
 Db 308 CATGACGCCAGCATCTACGTGTGCAGAGTGAGGTGCTGGGCCCTGGTGTGCGGACAGG 367
 Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
 Db 368 AATGGGACTCGGCTGGTGGTGGAGAAAGAAATCATCTCAGCTAGGGGCTGGTACAGTCC 427
 Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 Db 428 CTCCTTCGGGCTGGAATCTATGCTGTACGCTTCTCTGTGCGCGCTGGGAGCAGCCGTC 487
 Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
 Db 488 TATTACAGGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCTCAGATGGGCC 547
 Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
 Db 548 CGA-----GGRGTGATTCAGAGCCAGATGTGCC 577

RESULT 8
 US-10-036-444-1
 Sequence 1, Application US/10036444
 Publication No. US20020142445A1
 GENERAL INFORMATION:
 APPLICANT: INNATE PHARMA S.A.S.
 TITLE OF INVENTION: "Novel triggering receptor involved in natural
 TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
 TITLE OF INVENTION: antibodies that identify the same"
 FILE REFERENCE: SEQ-PR-1060
 CURRENT APPLICATION NUMBER: US/10/036,444
 CURRENT FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: 09/440,514
 PRIOR FILING DATE: 1999-11-15
 PRIOR APPLICATION NUMBER: 09/456,199
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 674
 TYPE: DNA
 ORGANISM: Human NK cell
 US-10-036-444-1

Alignment Scores:
 Pred. No.: 3,69e-93 Length: 674
 Score: 876.00 Matches: 173
 Percent Similarity: 90.2% Conservative: 2
 Best Local Similarity: 89.2% Mismatches: 7
 Query Match: 82.1% Indels: 12
 DB: 5 Gaps: 2

US-10-696-259-6 (1-201) x US-10-036-444-1 (1-674)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
 Db 64 ATGGCCCTGGATGCTGTGCTCATCTTGATCATGGTCCATCCAGGATCTGTGCTCTCGG 123
 Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
 Db 124 GTGTCCACAGCCCTGAGATTGCTGACCTGGAAAGGATCTCTGCTTCTGCTCCCTGCTCC 183
 Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 Db 184 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTCCGAGATCAGGTG 243
 Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
 Db 244 GTTCCAGGGAAGGAGGTGAGGAATGGAAACCCAGAGTTCCAGGGCCGCTGGCCCACTT 303
 Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 304 GCTTCTCCGTTTCTCCATGACCAACAGGCTGAGCTGCATCCGGGAGCTGGAGGC 363
 Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
 Db 364 CATGACCCAGCATCTACGTGTGCAGAGTGAGGTGCTGGGCCCTGGTGTGCGGACAGG 423
 Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
 Db 424 AATGGGACTCGGCTGGTGGTGGAGAAAGAAATCATCTCAGCTAGGGGCTGGTACAGTCC 483
 Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 Db 484 CTCCTTCGGGCTGGAATCTATGCTGTGCTGAGCTTCTCTGTGCGCGCTGGGAGCAGCCGTC 543
 Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
 Db 544 TATTACAGGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCTCAGATGGGCC 603
 Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186

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Db 604 CGA-----GGGTGATTCAGAGCCACAGATGTCCC 633
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RESULT 9
US-11-137-649-1
; Sequence 1, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "Novel triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/11/137,649
; PRIORITY FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Human NK cell
US-11-137-649-1
Alignment Scores:
Pred. No.: 3,696-93 Length: 674
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 10 Gaps: 2
US-10-696-259-6 (1-201) x US-11-137-649-1 (1-674)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 64 ATGGCTCGATGCTGTTGCTCATCTTGATCATGCTGATGCTGATGCTGATGCTGCTGCTG 123
Qy 21 ValSerGlnProProGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 124 GTGTCCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 183
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Db 184 TTCAATGCCAGCCAGGAGAGACTGGCCATTGGCTCCGTCAGTGGTCCGAGATGAGGTG 243
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 244 GTTCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGCCGCTGGCCCTGCTT 303
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 304 GCTTCTTCCCTTCCCTCATGACACACAGGCTGAGTGCACATCCCGGAGCGTCGAGGC 363
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuLeuGlyValGlyThrGly 120
Db 364 CATGACGCCAGCATCATGCTGTCAGAGTGGAGGTGGTGGGCTTGGTGTGCGGACAGGG 423
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 424 AATGGGATCTCGGCTGGTGGTGGAGAAAGAAATCATCTCAGCTAGGCGGTGGTACAGTCTC 483
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 484 CTCCTTGGGGTGGATTCATGCTGCTAGCTTTCTCTGTGGCGGTGGGAGACCCGTC 543
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrThrTrpLysGlyPro 172
|||||
Db 544 TATTACCAGGGGCAATGCCACTGTACATGGGAACACACTGCCACTCTCTCAGATGGGCC 603
|||||
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
|||||
Db 604 CGA-----GGGTGATTCAGAGCCACAGATGTCCC 633
|||||
RESULT 10
US-10-322-696-28
; Sequence 28, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 22173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-696-28
Alignment Scores:
Pred. No.: 8,92e-91 Length: 22173
Score: 872.00 Matches: 191
Percent Similarity: 52.5% Conservative: 1
Best Local Similarity: 52.2% Mismatches: 2
Query Match: 81.7% Indels: 172
DB: 7 Gaps: 3
US-10-696-259-6 (1-201) x US-10-322-696-28 (1-22173)
Qy 3 TrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer 22
Db 2577 TGGTCTTCTCTCTG-----CCCCAGGATCTGTGTCTCTGGGTGTCC 2621
Qy 23 GlnProGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 42
Db 2622 CAGCCCCCTCAGATTCGTACCTTGAAGGATCTCTGCTTCTGCTGCTGCTGCTGCTCAAT 2681
Qy 43 AlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 62
Db 2682 GCCAGCCAGGAGACTGGCCATTGGCTCGCTCAGTGGTTCGAGATGAGGTGTCCA 2741
Qy 63 GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
Db 2742 GGGAGAGGTGAGGAATGGACCCAGAGTTCCAGGGGCCCTTGGCCCCACTTGTCTTCT 2801
Qy 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
Db 2802 TCCGTTTCTCTCATGACCACAGGCTGAGTGCACATCCGAGCGTGGAGGCCATGAC 2861
Qy 103 AlaSerIleTyrValCysArgValGluValLeuLeuGlyValGlyThrGlyHisAsnGly 122
Db 2862 GCCAGCATCTACGCTGTGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2921
Qy 123 ThrArgLeuValValGluLys----- 129
Db 2922 ACTCGGCTGTGTGGAGAAAGGTGAGATGCTGGAGGTGGTGTCTCTCTCTGGTGGAG 2981
Qy 129 ----- 129
Db 2982 GCCCAAGAGGCAATGTCTTGGAGGAGGATGTCTCTCTCTGAGGCCCTTCTCTCCCT 3041
Qy 130 -----GluHisProGly 133
Db 3042 GAGCCTGTGTGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3101
Qy 133 nLeuGlyAlaGlyThrValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 153
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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112201.9
; FILING DATE: 03-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kltts, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P8341-7073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: exon
; LOCATION: 48..162
; FEATURE:
; NAME/KEY: exon
; LOCATION: 544..652
; NAME/KEY: exon
; LOCATION: 1044..1162
; NAME/KEY: exon
; LOCATION: 1475..1567
; NAME/KEY: exon
; LOCATION: 1775..1797
; NAME/KEY: exon
; LOCATION: 2325..2709
US-08-973-544-1

Alignment Scores:
Pred. No.: 7,29e-80 Length: 5581
Score: 773.00 Matches: 181
Percent Similarity: 51.1% Conservative: 0
Best Local Similarity: 51.1% Mismatches: 4
Query Match: 72.4% Indels: 171
DB: 2 Gaps: 3

US-10-696-259-6 (1-201) x US-08-973-544-1 (1-5581)

Qy 16 SerCysAlaLeuTrpValSerGlnProGluLeuArgThrLeuGluGlySerSerAla 35
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Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
Db 3888 TTCTGCGCCCTCTCTTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCCACGTGG 3829
Qy 56 PheArgAspGluValValProGlyValGluValArgAsnGlyThrProGluPheArgGly 75
Db 3828 TTCCGAGATGAGTGGTTCCAGGAGAGAGGTGAGGAATGGAACCCAGATTTCAGGGGC 3769
Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
Db 3768 GCGCT---CCATCTGCTTCTCCCGTTTCTCCATGATCACCAGGCTGAGCTGCACATC 3713
Qy 96 ArgAspValArgGlyHisAspAla-SerIleTrpValCysArgValGluValLeuGlyLe 115
Db 3712 CGGACGTGCGAGGCCATGACGCCAGGCACTACGTGTGCAGAGTGGAGGTGCTGGGCCT 3653
Qy 115 uGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys----- 129
Db 3652 TGGTGTGGGACAGGGAATGGGACTCGGCTGGTGGAGAAAGGTGAGATGCTGGGAGG 3593
Qy 129 ----- 421

Db 3592 TGGTGTCTCTCTCTGGCTGGAGGCCCAAGAGCAATGTCTCTTGGGAGGCAGGGATGCTCC 3533
Qy 129 ----- 129
Db 3532 TCTGAGGCCCTTCCCTCCCTGAGCCTGTGTGCACTTCTTCCCAACCCCGTCTCCATT 3473
Qy 130 -----GluHisProGlnLeu-GlyAlaGlyThrValLeuLeuLeuArgAlaGlyP 146
Db 3472 GCCCATGTCAGACATCTCTCAGTAGGGGCTGGTACAGTCTCTCT-CTTCGGGCTGGAT 3414
Qy 146 heTyRAlaValSerPheLeuSerValAlaValGlySerThrValTyR-GlnGlyLysC 166
Db 3413 TCTATGCTGTCACTTCTCTGTGGCCGTGGGACACCGTCTATTACAGGGCAAT 3354
Qy 166 ys----- 166
Db 3353 GTGAGTAATGGAGCCAGGGGCAATAGTGGACGGATGGGAGGGGACGTAAGAGAGTGGGA 3294
Qy 166 ----- 166
Db 3293 GGAGGAGGACAGAGACCAGGAGAGAGAGCCCTCGGGACTGCACTGAGCAGCTCCT 3234
Qy 166 ----- 166
Db 3233 GTCCTCTCTGTGACCAAGGCCACTGTACATGGGAACACACTGCCACTCTCTCAGATGGCC 3174
Qy 166 ----- 166
Db 3173 CCGAGGAGTGATTCAGAGCCAGATGTCCCTAGTCTCTTCAAAAGAGCCCCAATAATC 3114
Qy 166 ----- 166
Db 3113 TGCCCCACCACCTAACTCTCATGAGTCTCAAGTGTCTTCTTCTCCATTCTCCAGATGCCA 3054
Qy 167 -----LeuThrTrp 169
Db 3053 AATCTACTCTCTCGGATTCGCCCACTCTGAACCTTTCCTCCACCAGGCTCTGACCTGG 2994
Qy 170 LysGlyProArgGlnLeuProAlaValValProAlaProLeuProProCysGly 189
Db 2993 AAAGGTCCAAAGAGGAGCTGCCGGCTGTGGTCCAGCGCCCTCCACCACCATGTGGG 2934
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; Sequence 10, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Human NK cell
US-10-036-444-10
Alignment Scores:
Pred. No.: 5.64e-76 Length: 421

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Db 241 GCTTCTTCCCGTTTCTCCATGACCAACCCAGGCTGAGCTGCACATCCGGGACGTGCGAGGC 300
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCTTGGTGTCTGGGACAGGG 360
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGly 135
Db 361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCCTCAGCTAGGG 405

Search completed: February 28, 2006, 07:27:06
Job time : 786 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 07:06:37 ; Search time 322 Seconds
(without alignments)
1331.074 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=bl0eum2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs04
-USER=US10696259 -CGN 1_1_220 @runat_27022006_123603_27334 -NCPUS=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:*
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11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	855	80.1	40000	8	US-10-995-561-13510 Sequence 13510, A
C 2	853.5	80.0	6853	12	US-11-122-329-89 Sequence 89, Appl
C 3	347	32.5	201	8	US-10-995-561-84078 Sequence 84078, A
C 4	308	28.9	201	8	US-10-995-561-84065 Sequence 84065, A

c	5	199	18.7	201	8	US-10-995-561-84088	Sequence 84088, A
c	6	195	18.3	201	8	US-10-995-561-83983	Sequence 83983, A
c	7	194	18.2	201	8	US-10-995-561-84144	Sequence 84144, A
c	8	193	18.1	201	8	US-10-995-561-84089	Sequence 84089, A
c	9	187	17.5	201	8	US-10-995-561-84082	Sequence 84082, A
c	10	154.5	14.5	201	8	US-10-995-561-84087	Sequence 84087, A
	11	122	11.4	2754	8	US-10-821-234-163	Sequence 163, Appl
	12	120	11.2	1107	12	US-11-000-688-10	Sequence 10, Appl
	13	115	10.8	724	12	US-11-136-527-3003	Sequence 3003, Ap
	14	113.5	10.6	2220	9	US-11-072-512-1739	Sequence 1739, Ap
	15	110.5	10.4	2467	12	US-11-080-991-107	Sequence 107, App
	16	110.5	10.4	2479	8	US-10-955-054A-50	Sequence 50, Appl
	17	106	9.9	2980	7	US-10-511-538-228	Sequence 228, App
	18	98	9.2	912	12	US-11-000-463-12	Sequence 12, Appl
	19	98	9.2	1650	9	US-11-072-512-1263	Sequence 1263, Ap
	20	98	9.2	2036	12	US-11-136-527-2698	Sequence 2698, Ap
	21	97.5	9.1	822	8	US-10-623-155-440	Sequence 440, App
	22	97	9.1	930	12	US-11-000-463-107	Sequence 107, App
	23	97	9.1	5130	8	US-10-453-372-409	Sequence 409, App
	24	97	9.1	5130	12	US-11-135-855-12	Sequence 12, Appl
	25	97	9.1	5158	12	US-11-135-855-13	Sequence 13, Appl
	26	96.5	9.0	705	12	US-11-139-499-1	Sequence 1, Appli
c	27	95	8.9	894	12	US-11-000-463-484	Sequence 484, App
	28	94.5	8.9	1825	12	US-11-000-463-579	Sequence 579, App
	29	94	8.8	531	6	US-09-925-065A-423935	Sequence 423935,
	30	94	8.8	600	12	US-11-136-527-7099	Sequence 7099, Ap
	31	94	8.8	870	8	US-10-276-233A-4	Sequence 4, Appli
	32	94	8.8	933	8	US-10-623-155-439	Sequence 439, App
	33	93.5	8.8	4406	9	US-11-072-512-979	Sequence 979, App
	34	93.5	8.8	4947	8	US-10-995-561-457	Sequence 457, App
	35	93.5	8.8	6719	8	US-10-995-561-456	Sequence 456, App
	36	93	8.7	1019	8	US-10-775-169-232	Sequence 232, App
c	37	92.5	8.7	998	8	US-10-750-185-45237	Sequence 45237, A
c	38	92.5	8.7	998	8	US-10-750-623-45237	Sequence 45237, A
	39	92.5	8.7	5103	8	US-10-453-372-397	Sequence 397, App
	40	92.5	8.7	5103	8	US-10-453-372-411	Sequence 411, App
	41	92.5	8.7	5103	8	US-10-453-372-413	Sequence 413, App
	42	92.5	8.7	5103	8	US-10-453-372-415	Sequence 415, App
	43	92.5	8.7	5103	8	US-10-453-372-417	Sequence 417, App
	44	92	8.6	648	8	US-10-374-954-6	Sequence 6, Appli
	45	92	8.6	971	5	US-09-978-360A-214	Sequence 214, App

ALIGNMENTS

RESULT 1

US-10-995-561-13510/c
; Sequence 13510, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13510
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13510

Alignment Scores:
Pred. No.: 7.97e-63
Score: 855.00
Length: 40000
Matches: 188
Percent Similarity: 51.6%
Conservative: 1

Best Local Similarity:	51.4%	Mismatches:	5
Query Match:	80.1%	Indels:	172
DB:	8	Gaps:	3
US-10-696-259-6 (1-201) x US-10-995-561-13510 (1-40000)			
Qy	3	TrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer	22
Db	34893	TGGGTCTTCCTCTG-----CCCCAGGATCTGTGCTCTCTGGGTGCC	34849
Qy	23	GlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn	42
Db	34848	CAGCCCTCGAGATTCGTACCTGGAAGATCCTCTGCCCTCTGCCCTGCTCCTCAAT	34789
Qy	43	AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValPro	62
Db	34788	GCCAGCCAAAGGAGACTGGCATTGGCTCYGTACGTGTTCCGAGATGAGGTGTTCCA	34729
Qy	63	GlyLysGluValArgAsnGlyThrProGluPheArgGlyValGLeuAlaProLeuAlaSer	82
Db	34728	GGGAGGAGGTGAGGAATGGAAACCCAGATTCAGGGCCGCTTGCCCCACTTGCCTTCT	34669
Qy	83	SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp	102
Db	34668	TCCCGTTCTCCATGACCACACAGGCTGAGTGCAATCCGGAGCGTGCAGGCCATGAC	34609
Qy	103	AlaSerIleTyValCysArgValGluValLeuGlyLeuGlyValGlyThrGlyAsnGly	122
Db	34608	RCCAGATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTTGGTGTGGGACAGGGAATGG	34549
Qy	123	ThrArgLeuValValGlu-Lys-----	129
Db	34548	ACTCGCTGCTGTGGAGAAAGTGGAGATGCTGGGAGTGGTGTCTCTCTGGCTGGGAG	34489
Qy	129	-----	129
Db	34488	GCCCAAGAGGCAATGTCTTGGAGGCGAGGATGCTCTCTGAGGCCCTTCCCTCCCT	34429
Qy	130	-----GluHisProG1	133
Db	34428	GAGCTGTGTGACTTCTCCCAACCCCGTCTCATTTGCCCATGAGAACATCTCA	34369
Qy	133	nLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyAlaValSerPheLeuSe	153
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Qy	153	rValAlaValGlySerThrValTyTyGlnGlyLysCys-----	166
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Db	34188	AGAGGAGAGCTCGGACTGTCAACTGAGCAGCTCTGTCTCTCTCTGTGACGAGGCCAC	34129
Qy	166	-----	166
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Qy	166	-----	166
Db	34068	AGATGTCCCTAGTCTCTTTCAAAAGACCCCAATAAATCTGCCCCACCACCTAACTCCTCAT	34009
Qy	166	-----	166
Db	34008	GAGTCTCAAGTGTTCCTCTTCATTTCTCCAGATGCCAAATCTACTCTCTCGGATTCCTC	33949
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Db	33948	CCAACCTGTACTTTTCCCTTCCACCAGGTCTGACTGGAAAGGTCCAAGAAGKACAGTTC	33889

Qy	177	roAlaValValProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProp	197
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Db	33828	CAGTCCCGAGGGC 33815	
RESULT 2			
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; Sequence 89, Application US/11122329			
; Publication No. US20060019272A1			
; GENERAL INFORMATION:			
; APPLICANT: Geraci, Mark			
; APPLICANT: Bull, Todd			
; APPLICANT: Voelkel, Norbert			
; APPLICANT: Coldren, Chris			
; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gen			
; TITLE OF INVENTION: Expression Analysis of Peripheral Blood Cells			
; FILE REFERENCE: 2848-54			
; CURRENT APPLICATION NUMBER: US/11/122,329			
; CURRENT FILING DATE: 2005-05-03			
; PRIOR APPLICATION NUMBER: 60/568,129			
; PRIOR FILING DATE: 2004-05-03			
; NUMBER OF SEQ ID NOS: 128			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 89			
; LENGTH: 6853			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-122-329-89			
Alignment Scores:			
Pred. No.:	1.85e-63	Length:	6853
Score:	853.50	Matches:	186
Percent Similarity:	52.7%	Conservative:	0
Best Local Similarity:	52.7%	Mismatches:	0
Query Match:	80.0%	Indels:	167
DB:	12	Gaps:	2
US-10-696-259-6 (1-201) x US-11-122-329-89 (1-6853)			
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Db	5220	TCTGTGCTCTCTGGGTGCCAGCCCTTGAGATTCTGACCTCGAAGGATCTCTGTC	5161
Qy	36	PheLeuProCysSerPheAenAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp	55
Db	5160	TTCTGCGCTGCTCTTCAATGCCACCAAGGAGACTGGCCATTGGCTCCGTCACGTGG	5101
Qy	56	PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly	75
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Qy	76	ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle	95
Db	5040	CGCCTGGCCCCACTTGCTTCTCCGTTTCTCCATGACCCACCCAGGCTGAGCTGCACATC	4981
Qy	96	ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeu	115
Db	4980	CGGACGTGGAGGCCATGACCGCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTT	4921
Qy	116	GlyValGlyThrGlyAsnGlyThrArgLeuValValGlu-Lys-	129
Db	4920	GGTGTGGGACAGGAATGGACTCGCTGCTGTGTGGAGAAAGGTGAGATGCTGGGAGGT	4861
Qy	129	-----	129
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Qy	129	-----	129

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Db 4740 GCCCATGACAGAAATCTCAGCTAGGGCTGGTACAGTCTCTCTCTCTGGGCTGGATT 4681
Qy 146 eTyrAlaValSerPheLeuSerValAlaValGlySerThrValTyrThrGlnGlyLysCy 166
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Qy 166 s-----166
Db 4620 TGAGTAATGAGCCAGGGGCAATAGTGGACGGGATGGAGGGGCGAGTAAGAGAGTGGAG 4561
Qy 166 -----166
Db 4560 GAGGAGGACAGACAGACAGAGAGAGAGAGGCTCGGGACTGCAACACTGACAGCTCTG 4501
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Qy 166 -----166
Db 4440 CGAGGAGTATCCAGAGCCAGATGCTCCTAGTCTCTTCAAAAGACCCCAATAATCT 4381
Qy 166 -----166
Db 4380 GCCCACCACCTAATCTCTCATGAGTCTCAAGTGTCTTCTCTCCATCTCCAGATGCCA 4321
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Db 4260 AAGTCCCAAGAGGAGCAGTCCGCTGTGGTCCAGCGCCCTCCACCAACCATGTGGGA 4201
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RESULT 3
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; Sequence 84078, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84078
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84078
Alignment Scores:
Pred. No.: 2,36e-21 Length: 201
Score: 347.00 Matches: 66
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 32.5% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84078 (1-201)
Qy 20 TrpValSerGlnProProGluIleArgThrLeuGlySerSerAlaPheLeuProCys 39
```

```
Db 199 TGGGTGCCAGCCCTGAGATTGCTACCTCGAAGGATCCTCTGCTCTCTCTGCTGC 140
Qy 40 SerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGlu 59
Db 139 TCCTTCATGCCAGCCAGGAGGAGACTGGCCATTGGCTCTCTCAGTGTGTTCCGAGATGAG 80
Qy 60 ValValProGlyLysGluValAlaArgAsnGlyThrProGluPheArgGlyArgLeuAlaPro 79
Db 79 GTGGTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCCGCTGGCCCA 20
Qy 80 LeuAlaSerSerArgPhe 85
Db 19 CTGCTTCTTCTCCCGTTTC 2

RESULT 4
US-10-995-561-84065/c
; Sequence 84065, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84065
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84065
Alignment Scores:
Pred. No.: 5.41e-18 Length: 201
Score: 308.00 Matches: 59
Percent Similarity: 98.3% Conservative: 0
Best Local Similarity: 98.3% Mismatches: 1
Query Match: 28.9% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84065 (1-201)
Qy 70 ThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHis 89
Db 200 ACCCCAGAGTTCAGGGCCGCTGGCCCACTTGTCTTCTCCGTTTCTCCATGACCAC 141
Qy 90 GlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArg 109
Db 140 CAGGCTGAGTGCACATCCGGAGCGTGGAGGCCATGACRCCAGCATCTACGTGTGCAGA 81
Qy 110 ValGluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValGluLys 129
Db 80 GTGAGGTGCTGGGCTTGTGTGGGACAGGGAATGGGACTCGGCTGTGTGGAGAAA 21

RESULT 5
US-10-995-561-84088/c
; Sequence 84088, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84088
; LENGTH: 201
```

```
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-84088

Alignment Scores:
Pred. No.: 1.33e-08 Length: 201
Score: 199.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.7% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84088 (1-201)
Qy 167 LeuThrTrpLysGlyProArgGlnLeuProAlaValProLeuProPro 186
Db 130 CTGACCTGGAAAGGTCGAAGAGGAGCTCCGGCTGTGGTCCAGCGCCCTCCACCA 71
Qy 187 ProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 70 CCATGTGGAGCTCAGCACATCTGCTTCCCGCCAGTCCAGGAGGC 26

RESULT 6
US-10-995-561-83983/c
/ Sequence 83983, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 83983
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83983

Alignment Scores:
Pred. No.: 2.94e-08 Length: 201
Score: 195.00 Matches: 34
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.3% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-83983 (1-201)
Qy 168 ThrTrpLysGlyProArgGlnLeuProAlaValProAlaProLeuProPro 187
Db 199 ACCTGGAAAGTCCAAAGAGGACGCTCCGCTGTGGTCCAGCGCCCTCCACCA 140
Qy 188 CysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 139 TGTGGAGCTCAGCACATCTGCTTCCCGCCAGTCCAGGAGGC 98

RESULT 7
US-10-995-561-84144/c
/ Sequence 84144, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 84144
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-84144

Alignment Scores:
Pred. No.: 3.59e-08 Length: 201
Score: 194.00 Matches: 38
Percent Similarity: 95.0% Conservative: 0
Best Local Similarity: 95.0% Mismatches: 2
Query Match: 18.2% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84144 (1-201)
Qy 130 GluHisProGlnLeuGlyAlaGlyThrValLeuLeuArgAlaGlyPheTyAlaVal 149
Db 136 GAACATCCTCAGCTAGGGCTGGTACAGTCTCTWCTTGGGCTGGATTCTATGCTGTC 77
Qy 150 SerPheLeuSerValAlaValGlySerThrValTyTyGlnGlyLysCysLeuThrTrp 169
Db 76 AGCTTCTCTCTGTGGCCGTGGCAGCACCGTCTATTACCAGGCAAAATGTGAGTAATGG 17

RESULT 8
US-10-995-561-84089/c
/ Sequence 84089, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 84089
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-84089

Alignment Scores:
Pred. No.: 4.38e-08 Length: 201
Score: 193.00 Matches: 34
Percent Similarity: 97.1% Conservative: 0
Best Local Similarity: 97.1% Mismatches: 1
Query Match: 18.1% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84089 (1-201)
Qy 167 LeuThrTrpLysGlyProArgGlnLeuProAlaValProAlaProLeuProPro 186
Db 124 CTGACCTGGAAAGTCCAAAGAGGACGCTCCGCTGTGGTCCAGCGCCCTCCACCA 65
Qy 187 ProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 64 CCATGTGGAGCTCAGCACATCTGCTTCCCGCCAGTCCAGGAGGC 20

RESULT 9
US-10-995-561-84082/c
/ Sequence 84082, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
```

```
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84082
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84082

Alignment Scores:
Pred. No.: 1,44e-07 Length: 201
Score: 187.00 Matches: 37
Percent Similarity: 92.5% Conservatives: 0
Best Local Similarity: 92.5% Mismatches: 3
Query Match: 17.5% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84082 (1-201)

Qy 130 GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaVal 149
Db 183 GAACATCTCAGCTAGGCGGTGTACAGTCTCTCTCGGGCTGGATTCTATGCTGC 124

Qy 150 SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrp 169
Db 123 AGCTTTCTCTGTGCGCGTGGYGAGCAGCCGCTCTATTACCAGGGCAATGTGATATGG 64

RESULT 10
US-10-995-561-84087/c
; Sequence 84087, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84087
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84087

Alignment Scores:
Pred. No.: 9,08e-05 Length: 201
Score: 154.50 Matches: 31
Percent Similarity: 72.7% Conservatives: 1
Best Local Similarity: 70.5% Mismatches: 3
Query Match: 14.5% Indels: 9
DB: 8 Gaps: 1

US-10-696-259-6 (1-201) x US-10-995-561-84087 (1-201)

Qy 150 SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrp 169
Db 105 TCTGYACTTTCCCTTCCACCAAGT-----CTGACCTCG 73

Qy 170 LysGlyProArgGlnLeuProAlaValProAlaProLeuProProCysGly 189
Db 72 AAGGTCAGAGAGGAGCTGCGGCTGTGTGTCCTCCAGCGCCCTCCACCAACCATGTGGG 13

Qy 190 SerSerAlaHis 193
Db 12 AGCTCAGCAT 1

RESULT 11
US-10-821-234-163
; Sequence 163, Application US/10821234
```

```
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 163
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-163

Alignment Scores:
Pred. No.: 0.781 Length: 2754
Score: 122.00 Matches: 57
Percent Similarity: 37.2% Conservatives: 23
Best Local Similarity: 26.5% Mismatches: 92
Query Match: 11.4% Indels: 43
DB: 8 Gaps: 9

US-10-696-259-6 (1-201) x US-10-821-234-163 (1-2754)

Qy 2 AlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpVal 21
Db 296 GCCTGGCTGTGTCTGTCTACTGTCTGTGCATCATTTACAGCGCGTCCCGCGGTGAG 355

Qy 22 SerGlnProGluLeuLeuLeuLeuGlu---GlySerSerAlaPheLeuProCysSer 40
Db 356 CTGAGACCTTCAGACCTGTAAGTGTGTGGCGCAGACCAAACTGCCTCTGCTTC 415

Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValTrpPheArgAspGluVal 60
Db 416 TACCGAGGGGACTCCCGCGAG---CAAGTGGGCAAGTGGCATGGGCTCGGTGGACGG 472

Qy 61 ValProGly-----LysGluValArgAenGlyThrPro 71
Db 473 GCGCAAGGCGCCAGGAACTAGCGCTACTGCATCCAAATATACGGGCTTCATGTGAGCCG 532

Qy 72 GluPheArgGlyArgLeuAla-----ProLeuAlaSerSerArg 84
Db 533 GCTTACGAGGGCGCGTGGAGAGCGCGCCCGCCCAACCCCTCGGACGGCTCAGTG 592

Qy 85 PheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSer 104
Db 593 CTCCTG-----CGCAACGCGATGCGAGCGGATGAGGCG 625

Qy 105 IleTyrValCysArgValGluValLeuGlyValGlyThrGlyAenGlyThrArg 124
Db 626 GAGTACAGTGCCTGGGTGAGCACCTTCCCGCGCGAGCTTCCAGGCGCGGCTCGCGCTC 685

Qy 125 LeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAla 144
Db 686 CGAGTGTCTGGTCTCCCTCGCCCTCCTCACTGAATCTCTGGTCCAGCATAGAGAGGGCCAG 745

Qy 145 GlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGly 164
Db 746 GGC-----CTGACCTGGGAGCCCTCTCTGCACACT-----GAGGGC 781

Qy 165 Lys-----CysLeuThrTrp-----LysGly-ProArgArgGlnLeuPr 177
Db 782 AGCCCCAGCCCCAGCGTACCTGGGACACGAGGTCAAAGGCAACACGTCACGCGCTCC 841

Qy 177 oAlaValValProAlaProLeuProProCysGlySerSer 191
Db 842 TTCAAGCACTCCCGCTCTGTGCTGCGCTCACCTCAGAGTTCCACT 884
```


Qy 97 AspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu----- 113
Db 352 GGACTGAGGCTGCTGACACCGGACTGTACTTCTGCAAGGTGGAACTCATGTATCCACCG 411
Qy 114 GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGln 133
Db 412 CCATACTTTGTGGGCATGGGCAACGGGACCCAGTTTTRTGTATGATCCAGAACCATGC 471
Qy 134 LeuGlyAlaGlyThrValLeuLeuArgAla-----GlyPheTyrAlaVal 149
Db 472 CCAGATTCAGACTTCCTCTTGGATCCTGTGCTGAGTAGTTCGGGGTGTCTTCTAC 531
Qy 150 SerPheLeuSerValAlaValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrp 169
Db 532 AGTTTCTGTGTCACCGCTGTTCTTGAACAGGAGCGSTARGWMAAAGAGTCTCTTACA 591
Qy 170 LysGlyProArgGlnLeuProAlaValProAlaValProLeuProProCys 188
Db 592 ACAGGGGTCTATGTGAAATGCCC-----CCACAGAGCCAGAAATGT 633

RESULT 14

US-11-072-512-1739

; Sequence 1739, Application US/11072512

; Publication No. US20060029945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO

; APPLICANT: SEKI, NAOHICO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOTUKU

; APPLICANT: NAGAHARI, KENJI

; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: 084335-0191

; CURRENT APPLICATION NUMBER: US/11/072,512

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/350,978

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: JP 2001-379298

; PRIOR FILING DATE: 2001-11-05

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 1739

; LENGTH: 2220

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-072-512-1739

Alignment Scores:

Pred. No.: 3.4 Length: 2220

Score: 113.50

Percent Similarity: 37.4%

Best Local Similarity: 27.5%

Query Match: 10.6%

DB: 9

US-10-696-259-6 (1-201) x US-11-072-512-1739 (1-2220)

Qy 15 GlySerCysAlaLeuTrpValSerGlnPro-----ProGluIle 27
Db 707 GGGAAAGACGGGCTGGTGGTGTGAAGTCCCAACGATCGAGAAATGGCTCCAGACCTG 766

Qy 28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAanAlaSerGlnGlyArg 47
Db 767 TCCACCAACGAGGCTCCACGCGCTTCTTGCCTTGTCAAGGCGAGGGCGAGTCTCTGAG--- 823
Qy 48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg 67
Db 824 -----CCCAACATCACCTGGGCAAAAGAT----- 847
Qy 68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis 87
Db 848 -----GGCCAGCCTGTGTGGGCGCGGAGGGAAGTTTCAACATC 886
Qy 88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrVal 107
Db 887 CAGCCTTCTGGGAGTTGCTGGTGAAGAACTTGGAGGGCCAGGACGACGACCTATACC 946
Qy 108 CysArgValGlu---ValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuVal 126
Db 947 TGTACCGCTGAGAACCGCCGTGGGCGGGCCGCGCGCTGCACCTCACCATCCTCGGTA 1006
Qy 127 ValGluLys-GluHisProGlnLeuGly---AlaGlyThrValLeuLeuLeuArgAlaG1 145
Db 1007 CTGCCTGTGTTCACCACTTGGGACCGGACGCTGCGCTTGGGGACAGGCTGTGG 1066
Qy 145 yPhe-----TyrAlaValSerPheLeuSerValAlaVa 156
Db 1067 CTTCGCTGTGCAGCGGGGCGAGCCCACTCGCATTTGGTGGTCAACGACCGG 1126
Qy 156 lGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLe 176
Db 1127 CCAGTCACAGGTCTGGGTC-----TGCTGGGCATGGGTGGGACAGAGCCAGGAC 1177
Qy 176 uPro 177
Db 1178 ACCG 1181

RESULT 15

US-11-080-991-107

; Sequence 107, Application US/11080991

; Publication No. US20050266437A1

; GENERAL INFORMATION:

; APPLICANT: Veiby, Petter Ole

; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST

; TITLE OF INVENTION: AND OVARIAN CANCER

; FILE REFERENCE: MRI-039

; CURRENT APPLICATION NUMBER: US/11/080,991

; CURRENT FILING DATE: 2005-03-11

; PRIOR APPLICATION NUMBER: US/10/176,847

; PRIOR FILING DATE: 2002-06-21

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 107

; LENGTH: 2467

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc feature

; LOCATION: 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462,

; LOCATION: 2463, 2464, 2465, 2466, 2467

; OTHER INFORMATION: n = A,T,C or G

US-11-080-991-107

Alignment Scores:

Pred. No.: 6.85 Length: 2467

Score: 110.50

Percent Similarity: 34.0%

Best Local Similarity: 23.1%

Query Match: 10.4%

DB: 12

US-10-696-259-6 (1-201) x US-11-080-991-107 (1-2467)

Length: 2467
Matches: 57
Conservative: 27
Mismatch: 87
Indels: 76
Gaps: 10

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